

Appl. No. : 09/741,669
Filed : December 19, 2000

REMARKS

Claims 1-44, 57-127, 129-131 and 133 are cancelled. Claim 135 is newly added. Claims 45-56, 128 and 132-135 are pending, however, because claims 128 and 132 are withdrawn, only claims 45-56, 134 and 135 are currently presented for examination. Claim 45 is currently amended. Support for these amendments can be found in Table I at page 42, in Table II at page 50, in the claims as originally filed and elsewhere throughout the specification. As such, no new matter has been added to the application.

Applicants have reviewed the rejections of claims 45-56, 133 and 134 as set out in the instant Office Action. After careful consideration, Applicants respectfully traverse these rejections.

Information Disclosure Statements

Applicants would like to thank the Examiner for his prompt consideration of the references submitted with the Information Disclosure Statements filed on February 23, 2004 and March 16, 2004. However, in reviewing the returned copy of Form PTO-1449 that was filed on March 16, Applicants have noted that the Examiner has lined-out reference number two (PCT Publication WO01/02605) and stated that "no reference was provided." Applicants have reviewed the instant application's Image File Wrapper, which is available on the PAIR system, and have found this reference recorded as electronic image. Specifically, this reference is listed as a foreign document having a "Mail Room Date" of March 19, 2004. Given that this reference is part of the file wrapper for the instant application, Applicants respectfully request that the Examiner review this reference and provide Applicants with an initialed copy of Form PTO-1449.

Rejection of Claim 45 Under 35 U.S.C. § 112, Second Paragraph

The Examiner rejects claim 45 under 35 U.S.C. § 112, second paragraph as allegedly being vague and indefinite. In particular, the Examiner asserts that it is unclear whether the phrase "an antisense nucleic acid complementary to a nucleic acid" refers to the same molecule as the phrase "an antisense nucleic acid comprising a nucleotide sequence of SEQ ID NO: 60."

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Applicants have amended claim 45 so as to delete the phrase “an antisense nucleic acid comprising a nucleotide sequence of SEQ ID NO: 60.” Applicants respectfully submit that this amendment obviates the indefiniteness rejection.

In view of the foregoing claim amendment, Applicants request that the Examiner withdraw the rejection of claim 45 under 35 U.S.C. § 112, second paragraph.

Rejection of Claims 133 and 134 Under 35 U.S.C. § 112, First Paragraph – Written Description

The Examiner rejects claims 133 and 134 under 35 U.S.C. § 112, first paragraph as allegedly containing subject matter that was not described in the specification in such a way as to reasonably convey to one of ordinary skill in the art that Applicants possessed the claimed subject matter at the time the application was filed. In particular, the Examiner asserts that the specification fails to adequately describe nucleic acid sequences which encode a gene product having at least 70% amino acid identity to a gene product comprising the amino acid sequence of SEQ ID NO: 413.

Applicants maintain that both claims 133 and 134 are adequately supported by the specification. However, solely to expedite the issuance of the instant application, Applicants have cancelled claim 133. With respect to claim 134, Applicants note that this claim does not recite any language regarding nucleic acid sequences which encode a gene product having at least 70% amino acid identity to a gene product comprising the amino acid sequence of SEQ ID NO: 413 nor does it incorporate by reference a claim which recites such language. Claim 134 is dependent on claim 45 and recites the additional limitation that “said microbial cell is a Gram positive bacterium.” Because claim 134 does not recite the above-mentioned phrase regarding 70% homology, Applicants respectfully submit that this claim should not be subject to a rejection based on lack of adequate written description.

In view of the foregoing argument, Applicants respectfully request that the Examiner withdraw the rejection of claim 134 under 35 U.S.C. § 112, first paragraph.

Rejection of Claims 45-48, 50-56, 133 and 134 Under 35 U.S.C. § 112, First Paragraph – Enablement

The Examiner rejects claims 45-48, 50-56, 133 and 134 under 35 U.S.C. § 112, first paragraph as claiming subject matter which allegedly is not enabled by the specification. After

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carefully reviewing the instant Office Action, it appears that the Examiner is concerned that although the antisense nucleic acid of SEQ ID NO: 60 can be used to sensitize *E. coli* cells, it is unclear whether this same sequence can be used to sensitize **any kind of microbial cell**. In particular, the Examiner states that “the Applicant’s declaration filed under 37 C.F.R. § 1.132 filed on August 11, 2003 showed that a sensitized *E. coli* can be produced by expressing a sub-lethal level of an antisense nucleic acid comprising a nucleotide sequence of SEQ ID NO: 60. However, the specification does not provide a guidance to produce any kind of sensitized microbial cell as recited in claims 45-48 and 50-56. . . .” Specifically, the Examiner asserts that, “it is unclear whether SEQ ID NO: 60 can be used as an antisense nucleic acid in any kind of microbial cell as recited in claims 45-48, 50-56, 133 and 134 because the specification does not provide an [sic] evidence to show that SEQ ID NO: 60 is highly conserved in all microbial cell [sic] and can be used as an antisense nucleic acid in any kind of microbial cell.” In support of his assertions, the Examiner has provided BLAST search results (originally provided in the Office Action of January 8, 2004 but reiterated in the instant Office Action), which he alleges show that the nucleotide sequence of SEQ ID NO: 60 has substantial complementarity with only a limited number of microorganisms (see instant Office Action pages 8-9).

Applicants respectfully submit that claims 45-48, 50-56 and 134 have not been limited to the use of only an antisense nucleic acid of SEQ ID NO: 60 to sensitize microbial cells. Rather, each of these claims have been drawn to the use of any antisense nucleic acid capable of inhibiting the expression of a gene product encoded by the *yidC* gene. To clarify this point without narrowing the claims, Applicants have amended independent claim 45 to recite the step of “providing a sub-lethal level of an antisense nucleic acid so as to inhibit the expression of a *yidC* gene product in a microbial cell that comprises a *yidC* gene.” Applicants believe that this amendment addresses the Examiner’s concerns regarding the use of an antisense nucleic acid of **SEQ ID NO: 60** to sensitize **any microbial cell**. Specifically, this amendment clarifies that any antisense nucleic acid that inhibits the expression of a *yidC* gene product can be used to sensitize a microbial cell. Furthermore, the amended claim recites that only microbial cells which comprise a *yidC* gene are sensitized. Applicants respectfully submit that this amendment, in view of the following arguments, completely addresses the Examiner’s claim rejection based on lack of enablement.

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Claims 45-48, 50-56 and 134 are enabled by the instant specification. As currently amended, claim 45 recites a method for identifying a compound which reduces the activity or level of a gene product required for proliferation of a microorganism, said method comprising the steps of: (a) providing a sub-lethal level of an antisense nucleic acid so as to inhibit the expression of a *yidC* gene product in a microbial cell that comprises a *yidC* gene, thereby producing a sensitized microbial cell; (b) contacting said sensitized microbial cell with a compound; and (c) determining whether said compound inhibits the growth of said sensitized microbial cell. The instant specification teaches one of ordinary skill in the art how to practice this method without undue experimentation. As discussed further below, the specification explicitly describes (1) how to identify a *yidC* homolog in a microorganism having a *yidC* gene; and (2) how to obtain an antisense nucleic acid capable of inhibiting the expression of the product of the *yidC* homolog and how to use that antisense nucleic acid to sensitize the microbial cell from which the *yidC* homolog was identified.

With respect to the identification of *yidC* homologs, the specification provides extensive guidance which explains a routine method for identifying essential gene homologs from microorganisms other than *E. coli*. In particular, Applicants explicitly describe methods for identifying homologs of essential genes (e.g. the *yidC* gene) and/or essential gene products (e.g., the YidC protein) in microbial cells other than the one from which the essential gene was discovered. For example, the instant specification describes routine computer-based methods for identifying homologs of the *yidC* gene and YidC polypeptide in organisms other than *E. coli* (see page 31, line 9 to page 32, line 20 and page 40, line 20 to page 41, line 16, including Example 3). As an alternative to these computer-based methods, the specification also describes methods for identifying *yidC* coding sequences in organisms other than *E. coli* by using nucleic acid hybridization (see page 32, line 21 to page 34, line 5). As acknowledged by the Examiner, "the relative skill in the art is very high (the Ph.D. degree with laboratory experience)." In view of this high level of skill in the art, the above-described methods can be easily implemented without undue experimentation.

To demonstrate the routine nature of experimentation required to identify *yidC* homologs, Applicants' representative used the NCBI database to conduct both a word search for all *yidC* genes identified from microorganisms and a BLAST search using the full-length amino acid sequence of the YidC polypeptide from *E. coli* (SEQ ID NO: 413). The results of the word

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search indicated that YidC polypeptide have been identified from at least 188 different microorganisms (see Exhibit I). For almost all of these sequences, the corresponding *yidC* gene sequence has been determined and is readily accessible by following a hyperlink. The Blast search, which was limited to bacterial species for time and space efficiency, produced over 100 highly significant sequence hits (see Exhibit II). A review of the sequence alignments, which begins on page 7 of Exhibit B, reveals that several 60 kD YidC polypeptides from a wide array of microorganisms share substantial amino acid identity with the *E. coli* YidC polypeptide (SEQ ID NO: 413). As with the YidC polypeptides identified by word searching, nearly all of sequences discovered by BLAST searching are linked to their corresponding gene sequence.

In view of the foregoing results and arguments, Applicants respectfully submit that the identification of genes encoding YidC homologs from a wide range of microorganisms would not require undue experimentation.

Once a particular *yidC* homolog is identified in the desired microorganism, the procedures described in the specification can be readily used to identify antisense nucleic acids which inhibit the expression of the product of the *yidC* homolog. Such procedures are extensively described in the specification. In particular, the specification describes methods of using the nucleotide sequence of the homologous *yidC* gene as well as surrounding nucleotide sequence to generate antisense nucleic acids within or around the *yidC* homolog (see page 22, line 5 to page 24, line 26). Exemplary sizes and complementarity levels for these antisense nucleic acids are specifically described at page 30, lines 11 to 26. The antisense nucleic acids complementary to the *yidC* homolog as well as regions of sequence upstream and downstream thereto are then tested for their ability to inhibit the proliferation of the microbial cell that comprises the homologous *yidC* gene (see page 35, lines 22-27 and page 38, line 1 to page 40, line 19, including Examples 1 and 2; see also page 24, lines 16-26 and Example 4). Any of the antisense nucleic acids that inhibit proliferation of the microbial cell that comprises the homologous *yidC* gene can then be used to sensitize that cell in step (a) of claim 45 (see page 66, line 13 to page 79, line 11, including Examples 8 and 9).

Some instances may require that several antisense sequences be generated and tested as described above in order to identify particular antisense nucleic acids that are acceptable for use in the method of claim 45. However, the law is well established that experimentation is not undue even if considerable time and labor is required to achieve the desired result provided that

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the experimentation is routine to one of ordinary skill in the art. *In re Wands*. 858 F.2d 731 (Fed. Cir. 1988) (see also, *Johns Hopkins Univ. v. CellPro, Inc.*, 152 F.3d 1342, 1359 (Fed. Cir. 1998), which states that “a considerable amount of experimentation is permissible, if it is merely routine, or the specification in question provides a reasonable amount of guidance with respect to the direction in which the experimentation should proceed.”). Applicants respectfully submit that, in view of the level of skill in the art, generating antisense nucleic acids from a known essential gene sequence, transforming such antisense sequences into a microbial cell and determining whether the transformed cell’s proliferation is reduced as described in the specification is merely routine experimentation which is fully described in the instant specification.

In addition to the foregoing, Applicants have provided several actual examples of the identification of *yidC* antisense sequences that inhibit the expression of the essential *yidC* gene product and the use of these sequences in sensitized cell assays. For example, the instant specification provides an actual example of the use of the antisense nucleic acid of SEQ ID NO: 60 to sensitize *E. coli* cells. In addition, the Declaration under 37 C.F.R. § 1.132, which was filed on August 11, 2003 (a copy of which is provided herewith as Exhibit III), provides **two further examples** of independently identified antisense nucleic acids capable of inhibiting the expression of an essential *yidC* gene product in two unrelated microorganisms. In particular, the Declaration describes the identification of *yidC* antisense nucleic acids from a Gram positive bacterium and a Gram negative bacterium and the use of these antisense nucleic acids to inhibit the expression of the *yidC* gene product in the cells from which they were derived.

As set out in the Declaration, Applicants have (1) identified the YidC homolog in *Staphylococcus aureus*, (2) identified antisense nucleic acids capable of inhibiting the expression of the *yidC* gene product, and (3) shown that these antisense nucleic acids are capable of inhibiting the proliferation of (sensitizing) *Staphylococcus aureus*. These experiments, which are described in detail in the Declaration, were performed substantially as described in the instant application and were completed without difficulty. In particular, Applicants identified a number of different antisense nucleic acids complementary to the *S. aureus yidC* gene, which when expressed in *S. aureus*, inhibited its proliferation. Results of experiments in which the level of inhibitory antisense expression was varied, indicated that increasing the level of antisense expression increased the inhibition of proliferation (see Declaration).

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As a second example, the Declaration also describes a second inhibitory antisense nucleic acid obtained from *E. coli* (totally separate from and independent of SEQ ID NO: 60) which is complementary to at least a portion of the *yidC* gene. This second antisense nucleic acid, which was identified using the methods described in Examples 1 and 2 of the instant patent application, shares **no overlap** with SEQ ID NO: 60 but has the ability to inhibit *E. coli* proliferation to the same extent as SEQ ID NO: 60.

In view of the current claim amendments, the teachings provided in the specification and the Inventor's Declaration which confirms that inhibitory antisense nucleic acids complementary to *yidC* can be readily obtained without undue experimentation, Applicants maintain that Claims 45-48, 50-56 and 134 are enabled. As such, Applicants respectfully request that the Examiner withdraw his rejections of Claims 45-48, 50-56 and 134 under 35 U.S.C. § 112, first paragraph.

CONCLUSION


Applicants believe that all outstanding issues in this case have been resolved and that the present claims are in condition for allowance. Nevertheless, if any undeveloped issues remain or if any issues require clarification, the Examiner is invited to contact the undersigned at the telephone number provided below in order to expedite the resolution of such issues.

Please charge any additional fees, including any fees for additional extension of time, or credit overpayment to Deposit Account No. 11-1410.

Respectfully submitted,

KNOBBE, MARTENS, OLSON & BEAR, LLP

Dated: Nov. 12, 2004

By: 
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Attorney of Record
Customer No. 20,995
(619) 235-8550



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Nucleotide

Protein

Genome

Structure

PMC

Taxonomy

Boc

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Limits

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revision history

LinkOut

Related resources
BLASTReference sequence
project

Search for Genes

Clusters of orthologous
groupsProtein reviews on the
webSearch for full length
cDNAs

- ☐ 1: [AAU37088](#) Reports BLink, Domains, Links
YidC protein [Mannheimia succiniciproducens MBEL55E]
gi|52306588|gb|AAU37088.1|[52306588]
- ☐ 2: [NP_742176](#) Reports BLink, Domains, Links
inner membrane protein, 60 kDa [Pseudomonas putida KT2440]
gi|26986751|ref|NP_742176.1|[26986751]
- ☐ 3: [NP_246102](#) Reports BLink, Domains, Links
YidC [Pasteurella multocida subsp. multocida str. Pm70]
gi|15603030|ref|NP_246102.1|[15603030]
- ☐ 4: [YP_087673](#) Reports BLink, Domains, Links
YidC protein [Mannheimia succiniciproducens MBEL55E]
gi|52424536|ref|YP_087673.1|[52424536]
- ☐ 5: [YP_067050](#) Reports BLink, Domains, Links
60 kDa inner membrane protein [Rickettsia typhi str. Wilmington]
gi|51473293|ref|YP_067050.1|[51473293]
- ☐ 6: [YP_063241](#) Reports BLink, Domains, Links
preprotein translocase, YidC subunit [Leifsonia xyli subsp. xyli str.
CTCB07]
gi|50955953|ref|YP_063241.1|[50955953]
- ☐ 7: [YP_059641](#) Reports BLink, Domains, Links
60 kDa inner membrane protein [Streptococcus pyogenes MGAS10394]
gi|50913669|ref|YP_059641.1|[50913669]
- ☐ 8: [YP_059557](#) Reports BLink, Domains, Links
60 kDa inner membrane protein YIDC [Streptococcus pyogenes
MGAS10394]

gi|50913585|ref|YP_059557.1|[50913585]

☐ 9:

Reports

BLink, Domains, Links

YP_052530

putative membrane protein [Erwinia carotovora subsp. atroseptica
SCRI1043]

gi|50123363|ref|YP_052530.1|[50123363]

☐ 10:

Reports

BLink, Domains, Links

YP_016327

putative preprotein translocase subunit [Mycoplasma mobile 163K]

gi|47459465|ref|YP_016327.1|[47459465]

☐ 11:

Reports

BLink, Domains, Links

YP_008080

putative 60 kDa inner-membrane protein [Parachlamydia sp. UWE25]

gi|46446715|ref|YP_008080.1|[46446715]

☐ 12:

Reports

BLink, Domains, Links

NP_995271

probable membrane protein [Yersinia pestis biovar Medievalis str. 91001]

gi|45443732|ref|NP_995271.1|[45443732]

☐ 13:

Reports

BLink, Domains, Links

NP_970612

60 KD inner-membrane protein [Bdellovibrio bacteriovorus HD100]

gi|42525232|ref|NP_970612.1|[42525232]

☐ 14:

Reports

BLink, Domains, Links

NP_904074

integral membrane protein, 60 kDa [Chromobacterium violaceum ATCC
12472]

gi|34499859|ref|NP_904074.1|[34499859]

☐ 15:

Reports

BLink, Domains, Links

NP_878327

putative Preprotein translocase subunit YidC [Candidatus Blochmannia
floridanus]

gi|33519495|ref|NP_878327.1|[33519495]

☐ 16:

Reports

BLink, Domains, Links

NP_875693

Preprotein translocase subunit YidC [Prochlorococcus marinus subsp.
marinus str. CCMP1375]

gi|33240751|ref|NP_875693.1|[33240751]

☐ 17:

Reports

BLink, Domains, Links

NP_872666

60 kD inner-membrane protein [Haemophilus ducreyi 35000HP]

gi|33151313|ref|NP_872666.1|[33151313]

☐ 18:

Reports

BLink, Domains, Links

NP_868259

60 kDa inner-membrane protein homolog-putative part of a protein secretion system [*Rhodopirellula baltica* SH 1]

gi|32475265|ref|NP_868259.1|[32475265]

☐ 19:

Reports

BLink, Domains, Links

NP_852791

YidC [*Mycoplasma gallisepticum* R]

gi|31544213|ref|NP_852791.1|[31544213]

☐ 20:

Reports

BLink, Domains, Links

NP_839184

60 KD inner-membrane protein [*Shigella flexneri* 2a str. 2457T]

gi|30065013|ref|NP_839184.1|[30065013]

☐ 21:

Reports

BLink, Domains, Links

NP_835141

60 kDa inner membrane protein YIDC [*Bacillus cereus* ATCC 14579]

gi|30023510|ref|NP_835141.1|[30023510]

☐ 22:

Reports

BLink, Domains, Links

NP_834687

60 kDa inner membrane protein YIDC [*Bacillus cereus* ATCC 14579]

gi|30023056|ref|NP_834687.1|[30023056]

☐ 23:

Reports

BLink, Domains, Links

NP_807314

putative membrane protein [*Salmonella enterica* subsp. *enterica* serovar Typhi Ty2]

gi|29143972|ref|NP_807314.1|[29143972]

☐ 24:

Reports

BLink, Domains, Links

NP_777655

putative membrane protein [*Buchnera aphidicola* str. Bp (Baizongia pistaciae)]

gi|27904529|ref|NP_777655.1|[27904529]

☐ 25:

Reports

BLink, Domains, Links

NP_756486

60 kDa inner-membrane protein [*Escherichia coli* CFT073]

gi|26250446|ref|NP_756486.1|[26250446]

☐ 26:

Reports

BLink, Domains, Links

NP_709495

60 KD inner-membrane protein [*Shigella flexneri* 2a str. 301]

gi|24114985|ref|NP_709495.1|[24114985]

- ☐ **27:** Reports BLink, Links
NP_695955
truncated stage III sporulation protein J (SpoIIIJ) homolog [Bifidobacterium longum NCC2705]
gi|23465352|ref|NP_695955.1|[23465352]
- ☐ **28:** Reports BLink, Domains, Links
NP_695954
narrowly conserved hypothetical protein [Bifidobacterium longum NCC2705]
gi|23465351|ref|NP_695954.1|[23465351]
- ☐ **29:** Reports BLink, Domains, Links
NP_695830
conserved hypothetical transmembrane protein in the 60 kDa inner membrane protein family [Bifidobacterium longum NCC2705]
gi|23465227|ref|NP_695830.1|[23465227]
- ☐ **30:** Reports BLink, Domains, Links
NP_671407
60 kDa inner-membrane protein [Yersinia pestis KIM]
gi|22127984|ref|NP_671407.1|[22127984]
- ☐ **31:** Reports BLink, Domains, Links
NP_660377
inner membrane protein [Buchnera aphidicola str. Sg (Schizaphis graminum)]
gi|21672310|ref|NP_660377.1|[21672310]
- ☐ **32:** Reports BLink, Domains, Links
NP_624298
Preprotein translocase subunit YidC [Thermoanaerobacter tengcongensis]
gi|20809127|ref|NP_624298.1|[20809127]
- ☐ **33:** Reports BLink, Domains, Links
NP_602289
hypothetical protein NCgl2991 [Corynebacterium glutamicum ATCC 13032]
gi|19554287|ref|NP_602289.1|[19554287]
- ☐ **34:** Reports BLink, Domains, Links
NP_602127
hypothetical membrane protein [Corynebacterium glutamicum ATCC 13032]
gi|19554125|ref|NP_602127.1|[19554125]
- ☐ **35:** Reports BLink, Domains, Links
NP_541252
60 kDa inner membrane protein YidC [Brucella melitensis 16M]

gi|17988619|ref|NP_541252.1|[17988619]

☐ **36:** Reports BLink, Domains, Links
NP_462742

putative preprotein translocase subunit [Salmonella typhimurium LT2]
gi|16767127|ref|NP_462742.1|[16767127]

☐ **37:** Reports BLink, Domains, Links
NP_458101

putative membrane protein [Salmonella enterica subsp. enterica serovar Typhi str. CT18]
gi|16762484|ref|NP_458101.1|[16762484]

☐ **38:** Reports BLink, Domains, Links
NP_439163

inner membrane protein 60 kDa [Haemophilus influenzae Rd KW20]
gi|16272937|ref|NP_439163.1|[16272937]

☐ **39:** Reports BLink, Domains, Links
NP_418161

60 KD inner-membrane protein; preprotein translocase, cooperates with SecYE translocon, membrane component [Escherichia coli K12]
gi|16131573|ref|NP_418161.1|[16131573]

☐ **40:** Reports BLink, Domains, Links
NP_407523

probable membrane protein [Yersinia pestis CO92]
gi|16124210|ref|NP_407523.1|[16124210]

☐ **41:** Reports BLink, Domains, Links
NP_359711

60 kD inner-membrane protein [Rickettsia conorii str. Malish 7]
gi|15891997|ref|NP_359711.1|[15891997]

☐ **42:** Reports BLink, Domains, Links
NP_312667

60 KD inner-membrane protein [Escherichia coli O157:H7]
gi|15833894|ref|NP_312667.1|[15833894]

☐ **43:** Reports BLink, Domains, Links
NP_290338

60 KD inner-membrane protein [Escherichia coli O157:H7 EDL933]
gi|15804299|ref|NP_290338.1|[15804299]

☐ **44:** Reports BLink, Domains, Links
NP_266975

beta-glucosidase [Lactococcus lactis subsp. lactis II1403]
gi|15672801|ref|NP_266975.1|[15672801]

- ☐ **45:** Reports BLink, Domains, Links
NP_239857
60 kDa inner-membrane protein [Buchnera aphidicola str. APS (Acyrthosiphon pisum)]
gi|15616645|ref|NP_239857.1|[15616645]
- ☐ **46:** Reports BLink, Domains, Links
NP_220442
60 KD INNER-MEMBRANE PROTEIN (yidC) [Rickettsia prowazekii str. Madrid E]
gi|15603927|ref|NP_220442.1|[15603927]
- ☐ **47:** Reports BLink, Domains, Links
YP_072423
Oxa1 family transporter [Yersinia pseudotuberculosis IP 32953]
gi|51598232|ref|YP_072423.1|[51598232]
- ☐ **48:** Reports BLink, Domains, Links
Q8LBP4
Inner membrane protein ALBINO3, chloroplast precursor
gi|38372238|sp|Q8LBP4|ALB3_ARATH[38372238]
- ☐ **49:** Reports BLink, Domains, Links
ZP_00364739
COG0706: Preprotein translocase subunit YidC [Polaromonas sp. JS666]
gi|54032608|ref|ZP_00364739.1|[54032608]
- ☐ **50:** Reports BLink, Domains, Links
ZP_00018370
COG0706: Preprotein translocase subunit YidC [Chloroflexus aurantiacus]
gi|53799574|ref|ZP_00018370.2|[53799574]
- ☐ **51:** Reports BLink, Domains, Links
ZP_00038120
COG0706: Preprotein translocase subunit YidC [Xylella fastidiosa Dixon]
gi|22993537|ref|ZP_00038120.1|[22993537]
- ☐ **52:** Reports BLink, Domains, Links
ZP_00242356
COG0706: Preprotein translocase subunit YidC [Rubrivivax gelatinosus PM1]
gi|47572311|ref|ZP_00242356.1|[47572311]
- ☐ **53:** Reports BLink, Domains, Links
ZP_00211444
COG0706: Preprotein translocase subunit YidC [Burkholderia cepacia R18194]
gi|46310825|ref|ZP_00211444.1|[46310825]

- ☐ **54:** Reports BLink, Domains, Links
ZP_00210667
COG0706: Preprotein translocase subunit YidC [*Ehrlichia canis* str. Jake]
gi|46308474|ref|ZP_00210667.1|[46308474]
- ☐ **55:** Reports BLink, Domains, Links
ZP_00187017
COG0706: Preprotein translocase subunit YidC [*Rubrobacter xylanophilus*
DSM 9941]
gi|53765893|ref|ZP_00187017.2|[53765893]
- ☐ **56:** Reports BLink, Domains, Links
ZP_00167342
COG0706: Preprotein translocase subunit YidC [*Ralstonia eutropha*
JMP134]
gi|53761729|ref|ZP_00167342.2|[53761729]
- ☐ **57:** Reports BLink, Domains, Links
ZP_00350183
COG0706: Preprotein translocase subunit YidC [*Methylobacillus flagellatus*
KT]
gi|53759460|ref|ZP_00350183.1|[53759460]
- ☐ **58:** Reports BLink, Domains, Links
ZP_00226027
COG0706: Preprotein translocase subunit YidC [*Kineococcus radiotolerans*
SRS30216]
gi|46363258|ref|ZP_00226027.1|[46363258]
- ☐ **59:** Reports BLink, Domains, Links
ZP_00219032
COG0706: Preprotein translocase subunit YidC [*Burkholderia cepacia*
R1808]
gi|46318589|ref|ZP_00219032.1|[46318589]
- ☐ **60:** Reports BLink, Domains, Links
ZP_00162924
COG0706: Preprotein translocase subunit YidC [*Anabaena variabilis* ATCC
29413]
gi|46135472|ref|ZP_00162924.2|[46135472]
- ☐ **61:** Reports BLink, Domains, Links
ZP_00186768
COG0706: Preprotein translocase subunit YidC [*Rubrobacter xylanophilus*
DSM 9941]
gi|46106209|ref|ZP_00186768.2|[46106209]
- ☐ **62:** Reports BLink, Domains, Links
ZP_00192708

COG0706: Preprotein translocase subunit YidC [Mesorhizobium sp. BNC1]
gi|45681266|ref|ZP_00192708.1|[45681266]

☐ **63:** Reports BLink, Links
ZP_00164669
COG0706: Preprotein translocase subunit YidC [Synechococcus elongatus
PCC 7942]
gi|45513103|ref|ZP_00164669.1|[45513103]

☐ **64:** Reports BLink, Domains, Links
ZP_00156859
COG0706: Preprotein translocase subunit YidC [Haemophilus influenzae
R2866]
gi|46133236|ref|ZP_00156859.2|[46133236]

☐ **65:** Reports BLink, Domains, Links
ZP_00178122
COG0706: Preprotein translocase subunit YidC [Crocospaera watsonii
WH 8501]
gi|53735577|ref|ZP_00178122.2|[53735577]

☐ **66:** Reports BLink, Domains, Links
ZP_00133087
COG0706: Preprotein translocase subunit YidC [Haemophilus somnus
2336]
gi|53728372|ref|ZP_00133087.2|[53728372]

☐ **67:** Reports BLink, Links
ZP_00140183
COG0706: Preprotein translocase subunit YidC [Pseudomonas aeruginosa
UCBPP-PA14]
gi|53728245|ref|ZP_00140183.2|[53728245]

☐ **68:** Reports BLink, Domains, Links
ZP_00140404
COG0706: Preprotein translocase subunit YidC [Pseudomonas aeruginosa
UCBPP-PA14]
gi|53726901|ref|ZP_00140404.2|[53726901]

☐ **69:** Reports BLink, Links
ZP_00123372
COG0706: Preprotein translocase subunit YidC [Haemophilus somnus
129PT]
gi|53692334|ref|ZP_00123372.2|[53692334]

☐ **70:** Reports BLink, Domains, Links
ZP_00346395
COG0706: Preprotein translocase subunit YidC [Desulfovibrio
desulfuricans G20]

gi|53690668|ref|ZP_00346395.1|[53690668]

☐ **71:** Reports BLink, Domains, Links
ZP_00121168

COG0706: Preprotein translocase subunit YidC [*Bifidobacterium longum* DJO10A]

gi|46190726|ref|ZP_00121168.2|[46190726]

☐ **72:** Reports BLink, Links
ZP_00205929

COG0706: Preprotein translocase subunit YidC [*Pseudomonas syringae* pv. *syringae* B728a]

gi|46189160|ref|ZP_00205929.1|[46189160]

☐ **73:** Reports BLink, Domains, Links
ZP_00134946

COG0706: Preprotein translocase subunit YidC [*Actinobacillus pleuropneumoniae* serovar 1 str. 4074]

gi|46143583|ref|ZP_00134946.2|[46143583]

☐ **74:** Reports BLink, Domains, Links
ZP_00152752

COG0706: Preprotein translocase subunit YidC [*Dechloromonas aromatica* RCB]

gi|46140982|ref|ZP_00152752.2|[46140982]

☐ **75:** Reports BLink, Domains, Links
ZP_00201990

COG0706: Preprotein translocase subunit YidC [*Haemophilus influenzae* R2846]

gi|46129072|ref|ZP_00201990.1|[46129072]

☐ **76:** Reports BLink, Domains, Links
ZP_00153141

COG0706: Preprotein translocase subunit YidC [*Rickettsia rickettsii*]

gi|42453234|ref|ZP_00153141.1|[42453234]

☐ **77:** Reports BLink, Domains, Links
ZP_00124685

COG0706: Preprotein translocase subunit YidC [*Pseudomonas syringae* pv. *syringae* B728a]

gi|23469351|ref|ZP_00124685.1|[23469351]

☐ **78:** Reports BLink, Links
ZP_00101254

COG0706: Preprotein translocase subunit YidC [*Desulfitobacterium hafniense* DCB-2]

gi|53683292|ref|ZP_00101254.2|[53683292]

- ☐ **79:** Reports BLink, Domains, Links
ZP_00047349
COG0706: Preprotein translocase subunit YidC [*Lactobacillus gasseri*]
gi|52857817|ref|ZP_00047349.2|[52857817]
- ☐ **80:** Reports BLink, Domains, Links
ZP_00112140
COG0706: Preprotein translocase subunit YidC [*Nostoc punctiforme* PCC
73102]
gi|23130323|ref|ZP_00112140.1|[23130323]
- ☐ **81:** Reports BLink, Domains, Links
ZP_00091071
COG0706: Preprotein translocase subunit YidC [*Azotobacter vinelandii*]
gi|23104609|ref|ZP_00091071.1|[23104609]
- ☐ **82:** Reports BLink, Domains, Links
ZP_00063325
COG0706: Preprotein translocase subunit YidC [*Leuconostoc*
mesenteroides subsp. *mesenteroides* ATCC 8293]
gi|23024102|ref|ZP_00063325.1|[23024102]
- ☐ **83:** Reports BLink, Domains, Links
ZP_00063297
COG0706: Preprotein translocase subunit YidC [*Leuconostoc*
mesenteroides subsp. *mesenteroides* ATCC 8293]
gi|23024073|ref|ZP_00063297.1|[23024073]
- ☐ **84:** Reports BLink, Domains, Links
ZP_00055732
COG0706: Preprotein translocase subunit YidC [*Magnetospirillum*
magnetotacticum MS-1]
gi|23015970|ref|ZP_00055732.1|[23015970]
- ☐ **85:** Reports BLink, Domains, Links
ZP_00047201
COG0706: Preprotein translocase subunit YidC [*Lactobacillus gasseri*]
gi|23003541|ref|ZP_00047201.1|[23003541]
- ☐ **86:** Reports BLink, Domains, Links
ZP_00042125
COG0706: Preprotein translocase subunit YidC [*Xylella fastidiosa* Ann-1]
gi|22997918|ref|ZP_00042125.1|[22997918]
- ☐ **87:** Reports BLink, Domains, Links
ZP_00145659
COG0706: Preprotein translocase subunit YidC [*Psychrobacter* sp. 273-4]
gi|52853448|ref|ZP_00145659.2|[52853448]

- ☐ **88:** Reports BLink, Domains, Links
ZP_00207261
COG0706: Preprotein translocase subunit YidC [Rhodobacter sphaeroides 2.4.1]
gi|46192405|ref|ZP_00207261.1|[46192405]
- ☐ **89:** Reports BLink, Domains, Links
ZP_00006970
COG0706: Preprotein translocase subunit YidC [Rhodobacter sphaeroides 2.4.1]
gi|46192304|ref|ZP_00006970.2|[46192304]
- ☐ **90:** Reports BLink, Domains, Links
ZP_00339791
COG0706: Preprotein translocase subunit YidC [Rickettsia akari str. Hartford]
gi|52698383|ref|ZP_00339791.1|[52698383]
- ☐ **91:** Reports BLink, Domains, Links
NP_950501
preprotein translocase subunit YidC [Onion yellows phytoplasma OY-M]
gi|39938735|ref|NP_950501.1|[39938735]
- ☐ **92:** Reports BLink, Domains, Links
ZP_00338426
COG0706: Preprotein translocase subunit YidC [Silicibacter sp. TM1040]
gi|52011068|ref|ZP_00338426.1|[52011068]
- ☐ **93:** Reports BLink, Domains, Links
ZP_00334719
COG0706: Preprotein translocase subunit YidC [Thiobacillus denitrificans ATCC 25259]
gi|52007341|ref|ZP_00334719.1|[52007341]
- ☐ **94:** Reports BLink, Domains, Links
NP_871016
yidC [Wigglesworthia glossinidia endosymbiont of Glossina brevipalpis]
gi|32490762|ref|NP_871016.1|[32490762]
- ☐ **95:** Reports BLink, Domains, Links
AAT28116
putative preprotein translocase subunit [Mycoplasma mobile 163K]
gi|47458795|gb|AAT28116.1|[47458795]
- ☐ **96:** Reports BLink, Domains, Links
CAH23186
Oxa1 family transporter [Yersinia pseudotuberculosis IP 32953]
gi|51591514|emb|CAH23186.1|[51591514]

- ☐ **97:** Reports BLink, Domains, Links
XP_127742
oxidase assembly 1-like [Mus musculus]
gi|51768434|ref|XP_127742.3|[51768434]
- ☐ **98:** Reports BLink, Domains, Links
XP_485640
similar to hypothetical protein FLJ38991 [Mus musculus]
gi|51711053|ref|XP_485640.1|[51711053]
- ☐ **99:** Reports BLink, Domains, Links
AAU03568
60 kDa inner membrane protein [Rickettsia typhi str. Wilmington]
gi|51459605|gb|AAU03568.1|[51459605]
- ☐ **100:** Reports BLink, Domains, Links
AAL02612
60 kD inner-membrane protein [Rickettsia conorii str. Malish 7]
gi|15619112|gb|AAL02612.1|[15619112]
- ☐ **101:** Reports BLink, Domains, Links
NP_353415
AGR_C_674p [Agrobacterium tumefaciens str. C58]
gi|15887734|ref|NP_353415.1|[15887734]
- ☐ **102:** Reports BLink, Domains, Links
AAT90136
preprotein translocase, YidC subunit [Leifsonia xyli subsp. xyli str. CTCB07]
gi|50952435|gb|AAT90136.1|[50952435]
- ☐ **103:** Reports BLink, Domains, Links
AAT86458
60 kDa inner membrane protein [Streptococcus pyogenes MGAS10394]
gi|50902743|gb|AAT86458.1|[50902743]
- ☐ **104:** Reports BLink, Domains, Links
AAT86374
60 kDa inner membrane protein YIDC [Streptococcus pyogenes MGAS10394]
gi|50902659|gb|AAT86374.1|[50902659]
- ☐ **105:** Reports BLink, Domains, Links
XP_420604
PREDICTED: similar to hypothetical protein FLJ38991 [Gallus gallus]
gi|50746675|ref|XP_420604.1|[50746675]
- ☐ **106:** Reports BLink, Links
ZP_00332014

COG0706: Preprotein translocase subunit YidC [Streptococcus suis
89/1591]
gi|50590655|ref|ZP_00332014.1|[50590655]

☐ **107:** Reports BLink, Domains, Links
ZP_00331560
COG0706: Preprotein translocase subunit YidC [Streptococcus suis
89/1591]
gi|50590139|ref|ZP_00331560.1|[50590139]

☐ **108:** Reports BLink, Domains, Links
CAG77341
putative membrane protein [Erwinia carotovora subsp. atroseptica
SCRI1043]
gi|49613889|emb|CAG77341.1|[49613889]

☐ **109:** Reports BLink, Domains, Links
CAF23805
putative 60 kDa inner-membrane protein [Parachlamydia sp. UWE25]
gi|46400356|emb|CAF23805.1|[46400356]

☐ **110:** Reports BLink, Domains, Links
BAD04334
preprotein translocase subunit YidC [Onion yellows phytoplasma OY-M]
gi|39721844|dbj|BAD04334.1|[39721844]

☐ **111:** Reports BLink, Domains, Links
ZP_00329631
COG0706: Preprotein translocase subunit YidC [Moorella thermoacetica
ATCC 39073]
gi|49235564|ref|ZP_00329631.1|[49235564]

☐ **112:** Reports BLink, Domains, Links
AAC76728
60 KD inner-membrane protein; preprotein translocase, cooperates with
SecYE translocon, membrane component [Escherichia coli K12]
gi|1790140|gb|AAC76728.1|[1790140]

☐ **113:** Reports BLink, Domains, Links
ZP_00327996
COG0706: Preprotein translocase subunit YidC [Trichodesmium
erythraeum IMS101]
gi|48894887|ref|ZP_00327996.1|[48894887]

☐ **114:** Reports BLink, Domains, Links
ZP_00323511
COG0706: Preprotein translocase subunit YidC [Pediococcus pentosaceus
ATCC 25745]
gi|48870793|ref|ZP_00323511.1|[48870793]

- ☐ **115:** Reports BLink, Domains, Links
ZP_00323174
COG0706: Preprotein translocase subunit YidC [Pediococcus pentosaceus ATCC 25745]
gi|48870452|ref|ZP_00323174.1|[48870452]
- ☐ **116:** Reports BLink, Domains, Links
ZP_00321289
COG0706: Preprotein translocase subunit YidC [Haemophilus influenzae 86-028NP]
gi|48867865|ref|ZP_00321289.1|[48867865]
- ☐ **117:** Reports BLink, Links
ZP_00320335
COG0706: Preprotein translocase subunit YidC [Haemophilus influenzae 86-028NP]
gi|48866494|ref|ZP_00320335.1|[48866494]
- ☐ **118:** Reports BLink, Links
ZP_00320334
COG0706: Preprotein translocase subunit YidC [Haemophilus influenzae 86-028NP]
gi|48866493|ref|ZP_00320334.1|[48866493]
- ☐ **119:** Reports BLink, Domains, Links
ZP_00320215
COG0706: Preprotein translocase subunit YidC [Oenococcus oeni PSU-1]
gi|48866359|ref|ZP_00320215.1|[48866359]
- ☐ **120:** Reports BLink, Domains, Links
ZP_00318461
COG0706: Preprotein translocase subunit YidC [Microbulbifer degradans 2-40]
gi|48864568|ref|ZP_00318461.1|[48864568]
- ☐ **121:** Reports BLink, Domains, Links
ZP_00313558
COG0706: Preprotein translocase subunit YidC [Clostridium thermocellum ATCC 27405]
gi|48859626|ref|ZP_00313558.1|[48859626]
- ☐ **122:** Reports BLink, Domains, Links
ZP_00308560
COG0706: Preprotein translocase subunit YidC [Cytophaga hutchinsonii]
gi|48854398|ref|ZP_00308560.1|[48854398]
- ☐ **123:** Reports BLink, Domains, Links
ZP_00304958
COG0706: Preprotein translocase subunit YidC [Novosphingobium

aromaticivorans DSM 12444}
gi|48850716|ref|ZP_00304958.1|[48850716]

☐ **124:** Reports BLink, Domains, Links
ZP_00301338

COG0706: Preprotein translocase subunit YidC [Geobacter metallireducens GS-15]
gi|48847080|ref|ZP_00301338.1|[48847080]

☐ **125:** Reports BLink, Domains, Links
ZP_00292277

COG0706: Preprotein translocase subunit YidC [Thermobifida fusca]
gi|48835276|ref|ZP_00292277.1|[48835276]

☐ **126:** Reports BLink, Domains, Links
ZP_00291591

COG0706: Preprotein translocase subunit YidC [Thermobifida fusca]
gi|48834584|ref|ZP_00291591.1|[48834584]

☐ **127:** Reports BLink, Links
ZP_00291155

COG0706: Preprotein translocase subunit YidC [Magnetococcus sp. MC-1]
gi|48834140|ref|ZP_00291155.1|[48834140]

☐ **128:** Reports BLink, Domains, Links
ZP_00288574

COG0706: Preprotein translocase subunit YidC [Magnetococcus sp. MC-1]
gi|48831513|ref|ZP_00288574.1|[48831513]

☐ **129:** Reports BLink, Domains, Links
ZP_00285984

COG0706: Preprotein translocase subunit YidC [Enterococcus faecium]
gi|48824633|ref|ZP_00285984.1|[48824633]

☐ **130:** Reports BLink, Domains, Links
ZP_00277425

COG0706: Preprotein translocase subunit YidC [Burkholderia fungorum LB400]
gi|48780739|ref|ZP_00277425.1|[48780739]

☐ **131:** Reports BLink, Domains, Links
ZP_00275894

COG0706: Preprotein translocase subunit YidC [Ralstonia metallidurans CH34]
gi|48771552|ref|ZP_00275894.1|[48771552]

☐ **132:** Reports BLink, Domains, Links
ZP_00268613

COG0706: Preprotein translocase subunit YidC [Rhodospirillum rubrum]

gi|48764060|ref|ZP_00268613.1|[48764060]

☐ **133:**

AAK03249

Reports

BLink, Domains, Links

YidC [Pasteurella multocida subsp. multocida str. Pm70]
gi|12721513|gb|AAK03249.1|[12721513]

☐ **134:**

ZP_00265074

Reports

BLink, Domains, Links

COG0706: Preprotein translocase subunit YidC [Pseudomonas fluorescens PfO-1]
gi|48731329|ref|ZP_00265074.1|[48731329]

☐ **135:**

XP_391901

Reports

BLink, Domains, Links

similar to ENSANGP00000014070 [Apis mellifera]
gi|48097470|ref|XP_391901.1|[48097470]

☐ **136:**

CAF20964

Reports

BLink, Domains, Links

putative preprotein translocase subunit YidC, SpoIIJ homolog
[Corynebacterium glutamicum ATCC 13032]
gi|41327120|emb|CAF20964.1|[41327120]

☐ **137:**

CAF19036

Reports

BLink, Domains, Links

Preprotein translocase subunit YidC [Corynebacterium glutamicum ATCC 13032]
gi|41223091|emb|CAF19036.1|[41223091]

☐ **138:**

CAE81266

Reports

BLink, Domains, Links

60 KD inner-membrane protein [Bdellovibrio bacteriovorus HD100]
gi|39577443|emb|CAE81266.1|[39577443]

☐ **139:**

CAD83540

Reports

BLink, Domains, Links

putative Preprotein translocase subunit YidC [Candidatus Blochmannia floricola]
gi|33517158|emb|CAD83540.1|[33517158]

☐ **140:**

AAM25902

Reports

BLink, Domains, Links

Preprotein translocase subunit YidC [Thermoanaerobacter tengcongensis MB4]
gi|20517807|gb|AAM25902.1|[20517807]

☐ **141:**

NP_932057

Reports

BLink, Domains, Links

hypothetical protein [Photorhabdus luminescens subsp. laumondii TTO1]
gi|37528712|ref|NP_932057.1|[37528712]

☐ **142:** Reports BLink, Domains, Links
AAS64148

probable membrane protein [Yersinia pestis biovar Medievalis str. 91001]
gi|45438602|gb|AAS64148.1|[45438602]

☐ **143:** Reports BLink, Domains, Links
AAK04917

beta-glucosidase [Lactococcus lactis subsp. lactis II1403]
gi|12723742|gb|AAK04917.1|AE006315_6[12723742]

☐ **144:** Reports BLink, Domains, Links
AAC22663

inner membrane protein, 60 kDa (yidC) [Haemophilus influenzae Rd
KW20]
gi|1574032|gb|AAC22663.1|[1574032]

☐ **145:** Reports BLink, Domains, Links
AAK86200

AGR_C_674p [Agrobacterium tumefaciens str. C58]
gi|15155297|gb|AAK86200.1|[15155297]

☐ **146:** Reports BLink, Domains, Links
AAH01669

OXA1L protein [Homo sapiens]
gi|37589026|gb|AAH01669.2|[37589026]

☐ **147:** Reports BLink, Domains, MGC cDNA clone, Links
AAH27191

Oxa1l protein [Mus musculus]
gi|20073181|gb|AAH27191.1|[20073181]

☐ **148:** Reports BLink, Domains, Links
BAB38063

60 KD inner-membrane protein [Escherichia coli O157:H7]
gi|13364115|dbj|BAB38063.1|[13364115]

☐ **149:** Reports BLink, Domains, Links
BAC24159

yidC [Wigglesworthia glossinidia endosymbiont of Glossina brevipalpis]
gi|25165968|dbj|BAC24159.1|[25165968]

☐ **150:** Reports BLink, Domains, Links
P25714

Inner membrane protein oxaA
gi|398974|sp|P25714|OXAA_ECOLI[398974]

- ☐ **151:** Reports BLink, Domains, Links
XP_214011
similar to hypothetical protein FLJ38991 [Rattus norvegicus]
gi|34876681|ref|XP_214011.2|[34876681]
- ☐ **152:** Reports BLink, Domains, Links
XP_214182
similar to Cytochrome oxidase biogenesis protein OXA1, mitochondrial precursor (OXA1-like protein) (OXA1Hs) [Rattus norvegicus]
gi|34874107|ref|XP_214182.2|[34874107]
- ☐ **153:** Reports BLink, Domains, Links
AAQ62063
integral membrane protein, 60 kDa [Chromobacterium violaceum ATCC 12472]
gi|34332914|gb|AAQ62063.2|[34332914]
- ☐ **154:** Reports BLink, Domains, Links
CAE17278
unnamed protein product [Photorhabdus luminescens subsp. laumondii TTO1]
gi|36788151|emb|CAE17278.1|[36788151]
- ☐ **155:** Reports BLink, Domains, Links
ZP_00143985
60 kDa inner membrane protein YIDC [Fusobacterium nucleatum subsp. vincentii ATCC 49256]
gi|34763009|ref|ZP_00143985.1|[34763009]
- ☐ **156:** Reports BLink, Domains, Links
AAP56359
YidC [Mycoplasma gallisepticum R]
gi|31541057|gb|AAP56359.1|[31541057]
- ☐ **157:** Reports BLink, Domains, Links
AAP95055
60 kD inner-membrane protein [Haemophilus ducreyi 35000HP]
gi|33147533|gb|AAP95055.1|[33147533]
- ☐ **158:** Reports BLink, Links
AAN24591
truncated stage III sporulation protein J (SpoIIJ) homolog [Bifidobacterium longum NCC2705]
gi|23325994|gb|AAN24591.1|AE014699_12|[23325994]
- ☐ **159:** Reports BLink, Domains, Links
AAN24590
narrowly conserved hypothetical protein [Bifidobacterium longum NCC2705]

gi|23325993|gb|AAN24590.1|AE014699_11[23325993]

☐ 160:

AAN24466

Reports

BLink, Domains, Links

conserved hypothetical transmembrane protein in the 60 kDa inner membrane protein family [Bifidobacterium longum NCC2705]
gi|23325856|gb|AAN24466.1|AE014686_4[23325856]

☐ 161:

AAQ00346

Reports

BLink, Domains, Links

Preprotein translocase subunit YidC [Prochlorococcus marinus subsp. marinus str. CCMP1375]
gi|33238279|gb|AAQ00346.1|[33238279]

☐ 162:

CAD78537

Reports

BLink, Domains, Links

60 kDa inner-membrane protein homolog-putative part of a protein secretion system [Pirellula sp.]
gi|32445806|emb|CAD78537.1|[32445806]

☐ 163:

CAD03154

Reports

BLink, Domains, Links

putative membrane protein [Salmonella enterica subsp. enterica serovar Typhi]
gi|16504789|emb|CAD03154.1|[16504789]

☐ 164:

BAB12743

Reports

BLink, Domains, Links

60 kD inner-membrane protein [Buchnera aphidicola str. APS (Acyrtosiphon pisum)]
gi|10038708|dbj|BAB12743.1|[10038708]

☐ 165:

AAP12342

Reports

BLink, Domains, Links

60 kDa inner membrane protein YIDC [Bacillus cereus ATCC 14579]
gi|29899071|gb|AAP12342.1|[29899071]

☐ 166:

AAP11888

Reports

BLink, Domains, Links

60 kDa inner membrane protein YIDC [Bacillus cereus ATCC 14579]
gi|29898616|gb|AAP11888.1|[29898616]

☐ 167:

AAL22701

Reports

BLink, Domains, Links

putative preprotein translocase subunit YidC [Salmonella typhimurium LT2]
gi|16422416|gb|AAL22701.1|[16422416]

☐ 168:

Reports

BLink, Domains, Links

AAP18995

60 KD inner-membrane protein [Shigella flexneri 2a str. 2457T]

gi|30043274|gb|AAP18995.1|[30043274]

☐ 169:AAO71174

Reports

BLink, Domains, Links

putative membrane protein [Salmonella enterica subsp. enterica serovar Typhi Ty2]

gi|29139608|gb|AAO71174.1|[29139608]

☐ 170:AAO26760

Reports

BLink, Domains, Links

putative membrane protein [Buchnera aphidicola str. Bp (Baizongia pistaciae)]

gi|27903926|gb|AAO26760.1|[27903926]

☐ 171:AAL53516

Reports

BLink, Domains, Links

60 kDa inner membrane protein YidC [Brucella melitensis 16M]

gi|17984422|gb|AAL53516.1|[17984422]

☐ 172:AAG08953

Reports

BLink, Domains, Links

conserved hypothetical protein [Pseudomonas aeruginosa PAO1]

gi|9951909|gb|AAG08953.1|AE004968_7[9951909]

☐ 173:EAA24404

Reports

BLink, Domains, Links

60 kDa inner membrane protein YIDC [Fusobacterium nucleatum subsp. vincentii ATCC 49256]

gi|27887310|gb|EAA24404.1|[27887310]

☐ 174:AAN83060

Reports

BLink, Domains, Links

60 kDa inner-membrane protein [Escherichia coli CFT073]

gi|26110876|gb|AAN83060.1|AE016769_175[26110876]

☐ 175:AAN65640

Reports

BLink, Domains, Links

inner membrane protein, 60 kDa [Pseudomonas putida KT2440]

gi|24981341|gb|AAN65640.1|AE016190_6[24981341]

☐ 176:AI3543

Reports

BLink, Domains, Links

60K inner membrane protein yidC [imported] - Brucella melitensis (strain 16M)

gi|25299106|pir|AI3543[25299106]

☐ 177:

Reports

BLink, Domains, Links

G97405

60K inner-membrane protein (yidC) rp048 [imported] - Agrobacterium tumefaciens (strain C58, Cereon)
gi|25299104|pir||G97405[25299104]

☐ **178:**CAC93551

Reports

BLink, Domains, Links

probable membrane protein [Yersinia pestis CO92]
gi|15981991|emb|CAC93551.1|[15981991]

☐ **179:**H71712

Reports

BLink, Domains, Links

60 kd inner-membrane protein (yidC) RP048 - Rickettsia prowazekii
gi|7443251|pir||H71712[7443251]

☐ **180:**AAN45202

Reports

BLink, Domains, Links

60 KD inner-membrane protein [Shigella flexneri 2a str. 301]
gi|24054237|gb|AAN45202.1|AE015383_2[24054237]

☐ **181:**CAA14519

Reports

BLink, Domains, Links

60 KD INNER-MEMBRANE PROTEIN (yidC) [Rickettsia prowazekii]
gi|3860618|emb|CAA14519.1|[3860618]

☐ **182:**BAC00491

Reports

BLink, Domains, Links

Preprotein translocase subunit YidC [Corynebacterium glutamicum ATCC 13032]
gi|21325870|dbj|BAC00491.1|[21325870]

☐ **183:**BAC00334

Reports

BLink, Domains, Links

Preprotein translocase subunit YidC [Corynebacterium glutamicum ATCC 13032]
gi|21325713|dbj|BAC00334.1|[21325713]

☐ **184:**AAM87658

Reports

BLink, Domains, Links

60 kDa inner-membrane protein [Yersinia pestis KIM]
gi|21961130|gb|AAM87658.1|AE014013_3[21961130]

☐ **185:**AAM67588

Reports

BLink, Domains, Links

inner membrane protein [Buchnera aphidicola str. Sg (Schizaphis graminum)]
gi|21622909|gb|AAM67588.1|[21622909]

☐ **186:**

Reports

BLink, Domains, Links

AAL30086

60Kd inner-membrane protein [Xanthomonas campestris pv. campestris]
gi|21326646|gb|AAL30086.1|[21326646]

☐ **187:**

Reports

BLink, Domains, Links

AAG58902

60 KD inner-membrane protein [Escherichia coli O157:H7 EDL933]
gi|12518544|gb|AAG58902.1|AE005601_8[12518544]

☐ **188:**

Reports

BLink, Domains, Links

AAD56912

60KD inner-membrane protein yidC [Zymomonas mobilis]
gi|5932359|gb|AAD56912.1|AF180145_4[5932359]

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results of BLAST

BLASTP 2.2.10 [Oct-19-2004]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1099267621-14264-13688632949.BLASTQ4

Query=

(548 letters)

Database: Completed Aeropyrum pernix K1;
Completed Sulfolobus solfataricus P2;
Completed Sulfolobus tokodaii str. 7;
Completed Pyrobaculum aerophilum str. IM2;
Completed Archaeoglobus fulgidus DSM 4304;
Completed Halobacterium sp. NRC-1;
Completed Methanothermobacter thermautotrophicus str. Delta H;
Completed Methanocaldococcus jannaschii DSM 2661;
Completed Methanococcus maripaludis S2;
Completed Methanopyrus kandleri AV19;
Unfinished Methanococcoides burtonii DSM 6242; Completed Methanosarcina acetivorans
Unfinished Methanosarcina barkeri str. fusaro;
Completed Methanosarcina mazei Gol;
Completed Pyrococcus abyssi GE5;
Completed Pyrococcus furiosus DSM 3638;
Completed Pyrococcus horikoshii OT3;
Unfinished Ferroplasma acidarmanus;
Completed Picrophilus torridus DSM 9790;
Completed Thermoplasma acidophilum DSM 1728;
Completed Thermoplasma volcanium GSS1;
Completed Nanoarchaeum equitans Kin4-M;
Unfinished Bifidobacterium longum DJO10A;
Completed Bifidobacterium longum NCC2705;
Completed Corynebacterium diphtheriae NCTC 13129;
Completed Corynebacterium efficiens YS-314;
Completed Corynebacterium glutamicum ATCC 13032;
Unfinished Kineococcus radiotolerans SRS30216;
Completed Mycobacterium avium subsp. paratuberculosis str. k10;
Completed Mycobacterium bovis AF2122/97;
Completed Mycobacterium leprae TN;
Completed Mycobacterium tuberculosis CDC1551;
Completed Mycobacterium tuberculosis H37Rv;
Completed Nocardia farcinica IFM 10152;
Completed Propionibacterium acnes KPA171202;
Unfinished Rubrobacter xylanophilus DSM 9941;
Completed Streptomyces avermitilis MA-4680;
Completed Streptomyces coelicolor A3(2);
Completed Symbiobacterium thermophilum IAM 14863;
Unfinished Thermobifida fusca;
Completed Tropheryma whipplei TW08/27;
Completed Tropheryma whipplei str. Twist;

Completed Chlamydia muridarum;
Completed Chlamydia trachomatis D/UW-3/CX;
Completed Chlamydophila caviae GPIC;
Completed Chlamydophila pneumoniae AR39;
Completed Chlamydophila pneumoniae CWL029;
Completed Chlamydophila pneumoniae J138;
Completed Chlamydophila pneumoniae TW-183;
Completed Parachlamydia sp. UWE25;
Unfinished Anabaena variabilis ATCC 29413;
Unfinished Crocosphaera watsonii WH 8501;
Completed Gloeobacter violaceus PCC 7421;
Unfinished Nostoc punctiforme PCC 73102;
Completed Nostoc sp. PCC 7120;
Completed Prochlorococcus marinus str. MIT 9313;
Completed Prochlorococcus marinus subsp. marinus str. CCMP1375;
Completed Prochlorococcus marinus subsp. pastoris str. CCMP1986;
Unfinished Synechococcus elongatus PCC 7942;
Completed Synechococcus sp. WH 8102;
Completed Synechocystis sp. PCC 6803;
Completed Thermosynechococcus elongatus BP-1;
Unfinished Trichodesmium erythraeum IMS101;
Completed Bacillus anthracis str. 'Ames Ancestor';
Completed Bacillus anthracis str. A2012;
Completed Bacillus anthracis str. Ames;
Completed Bacillus anthracis str. Sterne;
Completed Bacillus cereus ATCC 10987;
Completed Bacillus cereus ATCC 14579;
Unfinished Bacillus cereus G9241;
Completed Bacillus cereus ZK;
Completed Bacillus halodurans C-125;
Completed Bacillus licheniformis DSM 13;
Completed Bacillus subtilis subsp. subtilis str. 168;
Completed Bacillus thuringiensis serovar konkukian str. 97-27;
Unfinished Exiguobacterium sp. 255-15;
Completed Listeria innocua Clip11262;
Completed Listeria monocytogenes EGD-e;
Unfinished Listeria monocytogenes str. 1/2a F6854;
Completed Listeria monocytogenes str. 4b F2365;
Unfinished Listeria monocytogenes str. 4b H7858;
Completed Oceanobacillus iheyensis HTE831;
Unfinished Pasteuria nishizawae str. North American;
Completed Staphylococcus aureus subsp. aureus MRSA252;
Completed Staphylococcus aureus subsp. aureus MSSA476;
Completed Staphylococcus aureus subsp. aureus MW2;
Completed Staphylococcus aureus subsp. aureus Mu50;
Completed Staphylococcus aureus subsp. aureus N315;
Completed Staphylococcus epidermidis ATCC 12228;
Completed Clostridium acetobutylicum ATCC 824;
Completed Clostridium perfringens str. 13;
Completed Clostridium tetani E88;
Unfinished Clostridium thermocellum ATCC 27405;
Unfinished Desulfitobacterium hafniense DCB-2;
Unfinished Moorella thermoacetica ATCC 39073;
Completed Thermoanaerobacter tengcongensis;
Completed Enterococcus faecalis V583;
Unfinished Enterococcus faecium;
Unfinished Lactobacillus gasseri;
Completed Lactobacillus johnsonii NCC 533;
Completed Lactobacillus plantarum WCFS1;
Completed Lactococcus lactis subsp. lactis I11403;

Unfinished *Leuconostoc mesenteroides* subsp. *mesenteroides* ATCC 8293;
Unfinished *Oenococcus oeni* PSU-1;
Unfinished *Pediococcus pentosaceus* ATCC 25745;
Completed *Streptococcus agalactiae* 2603V/R;
Completed *Streptococcus agalactiae* NEM316;
Completed *Streptococcus mutans* UA159;
Completed *Streptococcus pneumoniae* R6;
Completed *Streptococcus pneumoniae* TIGR4;
Completed *Streptococcus pyogenes* M1 GAS;
Completed *Streptococcus pyogenes* MGAS315;
Completed *Streptococcus pyogenes* MGAS8232;
Completed *Streptococcus pyogenes* SSI-1;
Unfinished *Streptococcus suis* 89/1591;
Completed *Mesoplasma florum* L1;
Completed *Mycoplasma gallisepticum* R;
Completed *Mycoplasma genitalium* G-37;
Completed *Mycoplasma hyopneumoniae* 232;
Completed *Mycoplasma mobile* 163K;
Completed *Mycoplasma mycoides* subsp. *mycoides* SC str. PG1;
Completed *Mycoplasma penetrans* HF-2;
Completed *Mycoplasma pneumoniae* M129;
Completed *Mycoplasma pulmonis* UAB CTIP;
Completed Onion yellows phytoplasma OY-M;
Completed *Ureaplasma parvum* serovar 3 str. ATCC 700970;
Completed *Aquifex aeolicus* VF5;
Completed *Bacteroides fragilis* YCH46;
Completed *Bacteroides thetaiotaomicron* VPI-5482;
Completed *Chlorobium tepidum* TLS;
Unfinished *Chloroflexus aurantiacus*;
Unfinished *Cytophaga hutchinsonii*;
Completed *Deinococcus radiodurans* R1;
Completed *Fusobacterium nucleatum* subsp. *nucleatum* ATCC 25586;
Unfinished *Fusobacterium nucleatum* subsp. *vincentii* ATCC 49256;
Completed *Porphyromonas gingivalis* W83;
Completed *Pirellula* sp. 1;
Completed *Thermotoga maritima* MSB8;
Completed *Thermus thermophilus* HB27;
Unfinished *Magnetococcus* sp. MC-1;
Completed *Bartonella henselae* str. Houston-1;
Completed *Bartonella quintana* str. Toulouse;
Completed *Bradyrhizobium japonicum* USDA 110;
Completed *Brucella melitensis* 16M;
Completed *Brucella suis* 1330;
Completed *Caulobacter crescentus* CB15;
Unfinished *Magnetospirillum magnetotacticum* MS-1;
Completed *Mesorhizobium loti* MAFF303099;
Unfinished *Mesorhizobium* sp. BNC1;
Unfinished *Novosphingobium aromaticivorans* DSM 12444;
Unfinished *Rhodobacter sphaeroides* 2.4.1;
Completed *Rhodopseudomonas palustris* CGA009;
Unfinished *Rhodospirillum rubrum*;
Unfinished *Silicibacter* sp. TM1040;
Completed *Agrobacterium tumefaciens* str. C58;
Completed *Sinorhizobium meliloti* 1021;
Unfinished *Ehrlichia canis* str. Jake;
Unfinished *Rickettsia akari* str. Hartford;
Completed *Rickettsia conorii* str. Malish 7;
Completed *Rickettsia prowazekii* str. Madrid E;
Unfinished *Rickettsia rickettsii*;
Unfinished *Rickettsia sibirica* 246;

Completed Wolbachia endosymbiont of Drosophila melanogaster;
Completed Bordetella bronchiseptica RB50;
Completed Bordetella parapertussis 12822;
Completed Bordetella pertussis Tohama I;
 Unfinished Burkholderia cepacia R1808;
 Unfinished Burkholderia cepacia R18194;
 Unfinished Burkholderia fungorum LB400;
Completed Burkholderia mallei ATCC 23344;
Completed Burkholderia pseudomallei K96243;
 Unfinished Ralstonia eutropha JMP134;
 Unfinished Ralstonia metallidurans CH34;
Completed Ralstonia solanacearum GMI1000;
Completed Chromobacterium violaceum ATCC 12472;
Completed Neisseria meningitidis MC58;
Completed Neisseria meningitidis Z2491;
 Unfinished Dechloromonas aromatica RCB;
 Unfinished Methylobacillus flagellatus KT;
Completed Nitrosomonas europaea ATCC 19718;
 Unfinished Polaromonas sp. JS666;
 Unfinished Rubrivivax gelatinosus PM1;
 Unfinished Thiobacillus denitrificans ATCC 25259;
Completed Bdellovibrio bacteriovorus HD100;
Completed Desulfotalea psychrophila LSV54;
 Unfinished Desulfovibrio desulfuricans G20;
Completed Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough;
 Unfinished Geobacter metallireducens GS-15;
Completed Geobacter sulfurreducens PCA;
Completed Campylobacter jejuni subsp. jejuni NCTC 11168;
Completed Helicobacter hepaticus ATCC 51449;
Completed Helicobacter pylori 26695;
Completed Helicobacter pylori J99;
Completed Wolinella succinogenes DSM 1740;
Completed Buchnera aphidicola str. APS (Acyrtosiphon pisum);
Completed Buchnera aphidicola str. Bp (Baizongia pistaciae);
Completed Buchnera aphidicola str. Sg (Schizaphis graminum);
Completed Candidatus Blochmannia floridanus;
Completed Escherichia coli CFT073;
Completed Escherichia coli K12;
Completed Escherichia coli O157:H7;
Completed Escherichia coli O157:H7 EDL933;
Completed Photobacterium luminescens subsp. laumondii TTO1;
Completed Salmonella enterica subsp. enterica serovar Typhi Ty2;
Completed Salmonella enterica subsp. enterica serovar Typhi str. CT18;
Completed Salmonella typhimurium LT2;
Completed Shigella flexneri 2a str. 2457T;
Completed Shigella flexneri 2a str. 301;
Completed Wigglesworthia glossinidia endosymbiont of Glossina brevipalpis;
Completed Yersinia pestis CO92;
Completed Yersinia pestis KIM;
Completed Yersinia pestis biovar Medievalis str. 91001;
Completed Yersinia pseudotuberculosis IP 32953;
Completed Coxiella burnetii RSA 493;
Completed Legionella pneumophila str. Lens;
Completed Legionella pneumophila str. Paris;
Completed Legionella pneumophila subsp. pneumophila str. Philadelphia 1;
Completed Methylococcus capsulatus str. Bath;
 Unfinished Microbulbifer degradans 2-40;
 Unfinished Psychrobacter sp. 273-4;
Completed Shewanella oneidensis MR-1;
 Unfinished Actinobacillus pleuropneumoniae serovar 1 str. 4074;

Completed Haemophilus ducreyi 35000HP;
Unfinished Haemophilus influenzae 86-028NP;
Unfinished Haemophilus influenzae R2846;
Unfinished Haemophilus influenzae R2866;
Completed Haemophilus influenzae Rd KW20;
Unfinished Haemophilus somnus 129PT;
Unfinished Haemophilus somnus 2336;
Completed Mannheimia succiniciproducens MBEL55E;
Completed Pasteurella multocida subsp. multocida str. Pm70;
Unfinished Azotobacter vinelandii;
Completed Pseudomonas aeruginosa PAO1;
Unfinished Pseudomonas aeruginosa UCBPP-PA14;
Unfinished Pseudomonas fluorescens PfO-1;
Completed Pseudomonas putida KT2440;
Unfinished Pseudomonas syringae pv. syringae B728a;
Completed Pseudomonas syringae pv. tomato str. DC3000;
Completed Photobacterium profundum SS9;
Completed Vibrio cholerae O1 biovar eltor str. N16961;
Completed Vibrio parahaemolyticus RIMD 2210633;
Completed Vibrio vulnificus CMCP6;
Completed Vibrio vulnificus YJ016;
Completed Xanthomonas axonopodis pv. citri str. 306;
Completed Xanthomonas campestris pv. campestris str. ATCC 33913;
Completed Xylella fastidiosa 9a5c;
Unfinished Xylella fastidiosa Ann-1;
Unfinished Xylella fastidiosa Dixon;
Completed Xylella fastidiosa Temecula1;
Completed Borrelia burgdorferi B31;
Completed Borrelia garinii PBI;
Completed Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130;
Completed Leptospira interrogans serovar Lai str. 56601;
Completed Treponema denticola ATCC 35405;
Completed Treponema pallidum subsp. pallidum str. Nichols;
Unfinished Ehrlichia ruminantium str. Welgevonden
 828,397 sequences; 254,881,094 total letters

If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)

Taxonomy reports

Sequences producing significant alignments:		Score (bits)	E Value
ref NP_418161.1	60 KD inner-membrane protein; preprotein t...	1110	0.0
ref NP_312667.1	60 KD inner-membrane protein [Escherichia ...	1109	0.0
ref NP_839184.1	60 KD inner-membrane protein [Shigella fle...	1106	0.0
ref NP_709495.1	60 KD inner-membrane protein [Shigella fle...	1078	0.0
ref NP_462742.1	putative preprotein translocase subunit [S...	1072	0.0
ref NP_458101.1	putative membrane protein [Salmonella ente...	1070	0.0
ref NP_407523.1	probable membrane protein [Yersinia pestis...	877	0.0
ref NP_932057.1	hypothetical protein [Photobacterium lumines...	850	0.0
ref NP_239857.1	60 kDa inner-membrane protein [Buchnera ap...	642	0.0
ref NP_796382.1	inner membrane protein, 60 kDa [Vibrio par...	622	e-177
ref NP_932796.1	inner membrane protein, 60 kDa [Vibrio vul...	620	e-177
ref NP_759968.1	Inner membrane protein, 60 kDa [Vibrio vul...	620	e-177
ref NP_660377.1	inner membrane protein [Buchnera aphidicol...	617	e-176
ref YP_087673.1	YidC protein [Mannheimia succiniciproducen...	617	e-176

ref NP_062588.1	inner membrane protein, 60 kDa [Vibrio cho...	614	e-175
ref YP_128260.1	Putative inner membrane protein, 60 kDa [P...	612	e-174
ref ZP_00201990.1	COG0706: Preprotein translocase subunit ...	607	e-173
ref NP_439163.1	inner membrane protein 60 kDa [Haemophilus...	607	e-172
ref ZP_00156859.2	COG0706: Preprotein translocase subunit ...	606	e-172
ref NP_246102.1	YidC [Pasteurella multocida subsp. multoci...	603	e-172
ref ZP_00134946.2	COG0706: Preprotein translocase subunit ...	602	e-171
ref NP_777655.1	putative membrane protein [Buchnera aphidi...	597	e-169
ref ZP_00133087.2	COG0706: Preprotein translocase subunit ...	592	e-168
ref NP_872666.1	60 kD inner-membrane protein [Haemophilus ...	589	e-167
ref NP_715646.1	inner membrane protein, 60 kDa [Shewanella...	570	e-161
ref NP_871016.1	yidC [Wigglesworthia glossinidia endosymbi...	538	e-152
ref NP_878327.1	putative Preprotein translocase subunit Yi...	528	e-149
ref ZP_00091071.1	COG0706: Preprotein translocase subunit ...	478	e-134
ref NP_742176.1	inner membrane protein, 60 kDa [Pseudomona...	475	e-133
ref ZP_00265074.1	COG0706: Preprotein translocase subunit ...	467	e-130
ref ZP_00124685.1	COG0706: Preprotein translocase subunit ...	461	e-129
ref NP_795330.1	inner membrane protein, 60 kDa [Pseudomona...	460	e-128
ref ZP_00140404.2	COG0706: Preprotein translocase subunit ...	446	e-124
ref NP_254255.1	hypothetical protein PA5568 [Pseudomonas a...	446	e-124
ref YP_115424.1	inner membrane protein, 60 kDa [Methylococ...	429	e-119
ref ZP_00145659.2	COG0706: Preprotein translocase subunit ...	428	e-119
ref YP_125376.1	hypothetical protein lpp3074 [Legionella p...	427	e-118
ref YP_096994.1	inner membrane protein, 60 kDa [Legionella...	426	e-118
ref NP_820897.1	inner-membrane protein, 60kDa [Coxiella bu...	426	e-118
ref YP_128254.1	hypothetical protein lpl2930 [Legionella p...	426	e-118
ref ZP_00350183.1	COG0706: Preprotein translocase subunit ...	418	e-116
ref ZP_00318461.1	COG0706: Preprotein translocase subunit ...	414	e-114
ref ZP_00152752.2	COG0706: Preprotein translocase subunit ...	406	e-112
ref NP_879348.1	probable inner-membrane protein [Bordetell...	385	e-106
ref ZP_00334719.1	COG0706: Preprotein translocase subunit ...	384	e-106
ref NP_891527.1	probable inner-membrane protein [Bordetell...	380	e-104
ref NP_886531.1	probable inner-membrane protein [Bordetell...	380	e-104
ref NP_840474.1	60Kd inner membrane protein [Nitrosomonas ...	379	e-104
ref ZP_00277425.1	COG0706: Preprotein translocase subunit ...	375	e-103
ref YP_106704.1	putative membrane protein [Burkholderia ps...	369	e-101
ref YP_104854.1	inner membrane protein, 60 kDa [Burkholder...	369	e-101
ref ZP_00242356.1	COG0706: Preprotein translocase subunit ...	365	e-100
ref ZP_00364739.1	COG0706: Preprotein translocase subunit ...	363	3e-99
ref ZP_00211444.1	COG0706: Preprotein translocase subunit ...	362	3e-99
ref NP_904074.1	integral membrane protein, 60 kDa [Chromob...	359	4e-98
ref ZP_00275894.1	COG0706: Preprotein translocase subunit ...	358	7e-98
ref ZP_00219032.1	COG0706: Preprotein translocase subunit ...	358	9e-98
ref NP_518125.1	PROBABLE TRANSMEMBRANE PROTEIN [Ralstonia ...	354	1e-96
ref ZP_00167342.2	COG0706: Preprotein translocase subunit ...	353	2e-96
ref NP_644666.1	60 kDa inner-membrane protein [Xanthomonas...	345	8e-94
ref NP_639574.1	60kDa inner-membrane protein [Xanthomonas ...	339	4e-92
ref NP_283364.1	putative integral membrane protein [Neisse...	331	9e-90
ref NP_274901.1	60 kd inner-membrane protein [Neisseria me...	330	1e-89
ref NP_780291.1	60 kDa inner-membrane protein [Xylella fas...	329	4e-89
ref ZP_00042125.1	COG0706: Preprotein translocase subunit ...	328	7e-89
ref NP_300057.1	60kDa inner-membrane protein [Xylella fast...	328	1e-88
ref ZP_00038120.1	COG0706: Preprotein translocase subunit ...	327	2e-88
ref NP_954506.1	membrane protein, putative [Geobacter sulf...	293	3e-78
ref ZP_00301338.1	COG0706: Preprotein translocase subunit ...	283	2e-75
ref ZP_00288574.1	COG0706: Preprotein translocase subunit ...	271	1e-71
ref NP_700186.1	inner-membrane protein, 60 kDa [Brucella s...	269	4e-71
ref NP_384550.1	PUTATIVE INNER-MEMBRANE TRANSMEMBRANE PROT...	266	4e-70
ref NP_541252.1	60 kDa inner membrane protein YidC [Brucel...	264	2e-69
ref ZP_00055732.1	COG0706: Preprotein translocase subunit ...	263	2e-69

ref YP_010298.1	inner membrane protein, 60 kDa [Desulfovib...	256	4e-67
ref ZP_00321289.1	COG0706: Preprotein translocase subunit ...	255	6e-67
ref NP_282110.1	putative membrane protein [Campylobacter j...	253	3e-66
ref NP_531090.1	60 kd inner-membrane protein [Agrobacteriu...	252	7e-66
ref ZP_00339791.1	COG0706: Preprotein translocase subunit ...	249	4e-65
ref NP_105597.1	hypothetical protein mlr4812 [Mesorhizobiu...	249	6e-65
gb EAA25857.1	60 kD inner-membrane protein [Rickettsia sib...	249	6e-65
ref NP_220442.1	60 KD INNER-MEMBRANE PROTEIN (yidC) [Ricke...	248	7e-65
ref NP_359711.1	60 kD inner-membrane protein [Rickettsia c...	248	1e-64
ref ZP_00192708.1	COG0706: Preprotein translocase subunit ...	248	1e-64
ref YP_064591.1	conserved hypothetical membrane protein [D...	246	5e-64
ref NP_774738.1	blr8098 [Bradyrhizobium japonicum USDA 110]	246	5e-64
ref ZP_00153141.1	COG0706: Preprotein translocase subunit ...	246	5e-64
ref ZP_00346395.1	COG0706: Preprotein translocase subunit ...	244	2e-63
ref ZP_00304958.1	COG0706: Preprotein translocase subunit ...	243	3e-63
ref NP_208241.1	60 kDa inner-membrane protein [Helicobacte...	242	7e-63
ref NP_907465.1	60 KDA INNER-MEMBRANE PROTEIN [Wolinella s...	241	2e-62
ref NP_224061.1	putative Inner membrane protein [Helicobac...	237	2e-61
ref NP_970612.1	60 KD inner-membrane protein [Bdellovibrio...	232	5e-60
ref NP_945985.1	60 kDa inner membrane protein [Rhodopseudo...	232	7e-60
ref ZP_00207261.1	COG0706: Preprotein translocase subunit ...	229	5e-59
ref ZP_00268613.1	COG0706: Preprotein translocase subunit ...	228	1e-58
ref YP_032573.1	hypothetical protein BQ09780 [Bartonella q...	226	3e-58
ref NP_859643.1	conserved hypothetical membrane protein [H...	223	3e-57
ref ZP_00338426.1	COG0706: Preprotein translocase subunit ...	220	3e-56
ref YP_033995.1	hypothetical protein BH12410 [Bartonella h...	212	6e-54

Alignments

>ref|NP_418161.1| 60 KD inner-membrane protein; preprotein translocase, cooperates
with SecYE translocon, membrane component [Escherichia
coli K12]
Length = 548

Score = 1110 bits (2871), Expect = 0.0
Identities = 548/548 (100%), Positives = 548/548 (100%)

Query: 1 MDSQRNLLVIALLFVSFMIWQAWQDKNPQPQAQQTQTQTTTTAAGSAADQGV PASGQGKL 60
MDSQRNLLVIALLFVSFMIWQAWQDKNPQPQAQQTQTQTTTTAAGSAADQGV PASGQGKL
Sbjct: 1 MDSQRNLLVIALLFVSFMIWQAWQDKNPQPQAQQTQTQTTTTAAGSAADQGV PASGQGKL 60

Query: 61 ISVKTDVLDLTINTRGGDVEQALLPAYPKELNSTQPFQLLETSPQFIYQAQSGLTGRDGP 120
ISVKTDVLDLTINTRGGDVEQALLPAYPKELNSTQPFQLLETSPQFIYQAQSGLTGRDGP
Sbjct: 61 ISVKTDVLDLTINTRGGDVEQALLPAYPKELNSTQPFQLLETSPQFIYQAQSGLTGRDGP 120

Query: 121 DNPANGPRPLYNVEKDAYVLAEGQNELQVPMTYTDAAGNTFTKT FVLKRGDYAVNVNYNV 180
DNPANGPRPLYNVEKDAYVLAEGQNELQVPMTYTDAAGNTFTKT FVLKRGDYAVNVNYNV
Sbjct: 121 DNPANGPRPLYNVEKDAYVLAEGQNELQVPMTYTDAAGNTFTKT FVLKRGDYAVNVNYNV 180

Query: 181 QNAGEKPLEISSFGQLKQSITLPPHLDTGSSNFALHTFRGAAYSTPDEKEYEKYKFDTIAD 240
QNAGEKPLEISSFGQLKQSITLPPHLDTGSSNFALHTFRGAAYSTPDEKEYEKYKFDTIAD
Sbjct: 181 QNAGEKPLEISSFGQLKQSITLPPHLDTGSSNFALHTFRGAAYSTPDEKEYEKYKFDTIAD 240

Query: 241 NENLNISSKGGWVAMLQQYFATAWI PHNDGTNNFYTANLGNIAAIGYKSQPVLVQPGQT 300
NENLNISSKGGWVAMLQQYFATAWI PHNDGTNNFYTANLGNIAAIGYKSQPVLVQPGQT
Sbjct: 241 NENLNISSKGGWVAMLQQYFATAWI PHNDGTNNFYTANLGNIAAIGYKSQPVLVQPGQT 300

Query: 301 GAMNSTLWVGPEIQDKMAAVAPHLDLTVDYGWLWFISQPLFKLLKWIHSFVGNWGFSSIII 360

Sbjct: 301 GAMNSTLWVGPEIQDKMAAVAPHLDLTVDYGWLWFISQPLFKLLKWIHSFVGNWGFSSIII 360

Query: 361 ITFIVRGIMYPLTKAQYTSMAKMRMLQPKIQAMRERLGDDKQRISQEMMALYKAKEVNPL 420
ITFIVRGIMYPLTKAQYTSMAKMRMLQPKIQAMRERLGDDKQRISQEMMALYKAKEVNPL

Sbjct: 361 ITFIVRGIMYPLTKAQYTSMAKMRMLQPKIQAMRERLGDDKQRISQEMMALYKAKEVNPL 420

Query: 421 GGCFLLIQMPIFLALYYMLMGVELRQAPFALWIHDLAQDPYYILPILMGVTMFFIQK 480
GGCFLLIQMPIFLALYYMLMGVELRQAPFALWIHDLAQDPYYILPILMGVTMFFIQK

Sbjct: 421 GGCFLLIQMPIFLALYYMLMGVELRQAPFALWIHDLAQDPYYILPILMGVTMFFIQK 480

Query: 481 MSPTTVDPMQKIMTFMPVIFTVFFLWFPSGLVLYYIVSNLVTIIQQQLIYRGLEKRG 540
MSPTTVDPMQKIMTFMPVIFTVFFLWFPSGLVLYYIVSNLVTIIQQQLIYRGLEKRG

Sbjct: 481 MSPTTVDPMQKIMTFMPVIFTVFFLWFPSGLVLYYIVSNLVTIIQQQLIYRGLEKRG 540

Query: 541 HSREKKKS 548
HSREKKKS

Sbjct: 541 HSREKKKS 548

>ref|NP_312667.1| 60 KD inner-membrane protein [Escherichia coli O157:H7]
ref|NP_756486.1| 60 kDa inner-membrane protein [Escherichia coli CFT073]
ref|NP_290338.1| 60 KD inner-membrane protein [Escherichia coli O157:H7 EDL933]
Length = 548

Score = 1109 bits (2868), Expect = 0.0
Identities = 547/548 (99%), Positives = 548/548 (100%)

Query: 1 MDSQRNLLVIALLFVSFMIWQAWQDKNPQQAQQTQTQTTTTAAGSAADQGV PASGQGKL 60
MDSQRNLLVIALLFVSFMIWQAWQDKNPQQAQQTQTQTTTTAAGSAADQGV PASGQGKL

Sbjct: 1 MDSQRNLLVIALLFVSFMIWQAWQDKNPQQAQQTQTQTTTTAAGSAADQGV PASGQGKL 60

Query: 61 ISVKTDVLDLTINTRGGDVEQALLPAYPKELNSTQPFQLETS PQFIYQAQSGLTGRDGP 120
ISVKTDVLDLTINTRGGDVEQALLPAYPKELNSTQPFQLETS PQFIYQAQSGLTGRDGP

Sbjct: 61 ISVKTDVLDLTINTRGGDVEQALLPAYPKELNSTQPFQLETS PQFIYQAQSGLTGRDGP 120

Query: 121 DNPANGPRPLYNVEKDAYVLAEGQNELQVPMTYTDAGNTFTKTFVLKRGDYAVNVNYNV 180
DNPANGPRPLYNVEKDAYVLAEGQNELQVPMTYTDAGNTFTKTFVLKRGDYAVNVNYNV

Sbjct: 121 DNPANGPRPLYNVEKDAYVLAEGQNELQVPMTYTDAGNTFTKTFVLKRGDYAVNVNYNV 180

Query: 181 QNAGEKPLEISSFGQLKQSITLPPHLDTGSSNFALHTFRGAAYSTPDEKYEKYKFDTIAD 240
QNAGEKPLEIS+FGQLKQSITLPPHLDTGSSNFALHTFRGAAYSTPDEKYEKYKFDTIAD

Sbjct: 181 QNAGEKPLEISTFGQLKQSITLPPHLDTGSSNFALHTFRGAAYSTPDEKYEKYKFDTIAD 240

Query: 241 NENLNISCKGGWVAMLQQYFATAWI PHNDGTNNFYTANLGNGIAAIGYKSQPV LVQPGQT 300
NENLNISCKGGWVAMLQQYFATAWI PHNDGTNNFYTANLGNGIAAIGYKSQPV LVQPGQT

Sbjct: 241 NENLNISCKGGWVAMLQQYFATAWI PHNDGTNNFYTANLGNGIAAIGYKSQPV LVQPGQT 300

Query: 301 GAMNSTLWVGPEIQDKMAAVAPHLDLTVDYGWLWFISQPLFKLLKWIHSFVGNWGFSSIII 360
GAMNSTLWVGPEIQDKMAAVAPHLDLTVDYGWLWFISQPLFKLLKWIHSFVGNWGFSSIII

Sbjct: 301 GAMNSTLWVGPEIQDKMAAVAPHLDLTVDYGWLWFISQPLFKLLKWIHSFVGNWGFSSIII 360

Query: 361 ITFIVRGIMYPLTKAQYTSMAKMRMLQPKIQAMRERLGDDKQRISQEMMALYKAKEVNPL 420
ITFIVRGIMYPLTKAQYTSMAKMRMLQPKIQAMRERLGDDKQRISQEMMALYKAKEVNPL

Sbjct: 361 ITFIVRGIMYPLTKAQYTSMAKMRMLQPKIQAMRERLGDDKQRISQEMMALYKAKEVNPL 420

Query: 421 GGCFLLIQMPIFLALYYMLMGVELRQAPFALWIHDLAQDPYYILPILMGVTMFFIQK 480
GGCFLLIQMPIFLALYYMLMGVELRQAPFALWIHDLAQDPYYILPILMGVTMFFIQK

Sbjct: 421 GGCFLLIQMPIFLALYYMLMGVELRQAPFALWIHDLAQDPYYILPILMGVTMFFIQK 480

Query: 481 MSPTTIVTDPMQQKIMTFMPVIFTVFFLWFPSGLVLYYIVSNLVTIIQQQLIYRGLEKRGL 540
MSPTTIVTDPMQQKIMTFMPVIFTVFFLWFPSGLVLYYIVSNLVTIIQQQLIYRGLEKRGL
Sbjct: 481 MSPTTIVTDPMQQKIMTFMPVIFTVFFLWFPSGLVLYYIVSNLVTIIQQQLIYRGLEKRGL 540

Query: 541 HSREKKKS 548
HSREKKKS
Sbjct: 541 HSREKKKS 548

>ref|NP_839184.1| 60 KD inner-membrane protein [Shigella flexneri 2a str. 2457T]
Length = 548

Score = 1106 bits (2861), Expect = 0.0
Identities = 546/548 (99%), Positives = 546/548 (99%)

Query: 1 MDSQRNLLVIALLFVSFMIWQAWEQDKNPQQAQQTQTQTTTTAAGSAADQGV PASGQGKL 60
MDSQRNLLVIALLFVSFMIWQAWEQDKNPQQAQQTQTQTTTTAAGSAADQGV PASGQGKL
Sbjct: 1 MDSQRNLLVIALLFVSFMIWQAWEQDKNPQQAQQTQTQTTTTAAGSAADQGV PASGQGKL 60

Query: 61 ISVKTDVLDLTINTRGGDVEQALLPAYPKELNSTQPFQLETS PQFIYQAQSGLTGRDGP 120
ISVKTDVLDLTINTRGGDVEQALLPAYPKELNSTQPFQLETS PQFIYQAQSGLTGRDGP
Sbjct: 61 ISVKTDVLDLTINTRGGDVEQALLPAYPKELNSTQPFQLETS PQFIYQAQSGLTGRDGP 120

Query: 121 DNPANGPRPLYNVEKDAYVLAEGQNELQVPMTYTDAAGNTFTKT FVLKRGDYAVNVNYNV 180
DNPANGPRPLYNVEKDAYVLAEGQNELQVPMTYTDAAGNTFTKT FVLKRGDYAVNVNYNV
Sbjct: 121 DNPANGPRPLYNVEKDAYVLAEGQNELQVPMTYTDAAGNTFTKT FVLKRGDYAVNVNYNV 180

Query: 181 QNAGEKPLEISSFGQLKQSITLPPHLDTGSSNFALHTFRGAAYSTPDEKEYEKYKFDTIAD 240
QNAGEKPLEISSFGQLKQSITLPPHLDTGSSNFALHTFRGAAYSTPDEKEYEKYKFDTIAD
Sbjct: 181 QNAGEKPLEISSFGQLKQSITLPPHLDTGSSNFALHTFRGAAYSTPDEKEYEKYKFDTIAD 240

Query: 241 NENLNIS SKGGWVAMLQQYFATAWI PHNDGTNNFY TANLNGIAAIGYKSQPVLVQPGQT 300
NENLNIS SKGGWVAMLQQYFATAWI PHNDGTNNFY TANLNGI AIGYKSQPVLVQPGQT
Sbjct: 241 NENLNIS SKGGWVAMLQQYFATAWI PHNDGTNNFY TANLNGIVAIGYKSQPVLVQPGQT 300

Query: 301 GAMNSTLWVGPEIQDKMAAVAPHLDLTVDYGWLWFISQPLFKLLKWIHSFVGNWGF SIII 360
GAMNSTLWVGPEIQDKMAAVAPHLDLTVDYGWLWFISQPLFKLLKWIHSFVGNWGF SIII
Sbjct: 301 GAMNSTLWVGPEIQDKMAAVAPHLDLTVDYGWLWFISQPLFKLLKWIHSFVGNWGF SIII 360

Query: 361 ITFIVRGIMYPLTKAQYTSMAKMRMLQPKIQAMRERLGDDKQRISQEMMALYKAEKVNPL 420
ITFIVRGIMYPLTKAQYTSMAKMRMLQPKIQAMRERLGDDKQRISQEMMALYKAEKVNPL
Sbjct: 361 ITFIVRGIMYPLTKAQYTSMAKMRMLQPKIQAMRERLGDDKQRISQEMMALYKAEKVNPL 420

Query: 421 GGCFFLLIQMPIFLALYYMLMG SVELRQAPFALWIHDLSAQDPYYILPILMGVTMFFIQK 480
GGCFFLLIQMPIFLALYYMLMG SVELRQAPFALWIHDLSAQDPYYILPILMGVTM FIQK
Sbjct: 421 GGCFFLLIQMPIFLALYYMLMG SVELRQAPFALWIHDLSAQDPYYILPILMGVTMLFIQK 480

Query: 481 MSPTTIVTDPMQQKIMTFMPVIFTVFFLWFPSGLVLYYIVSNLVTIIQQQLIYRGLEKRGL 540
MSPTTIVTDPMQQKIMTFMPVIFTVFFLWFPSGLVLYYIVSNLVTIIQQQLIYRGLEKRGL
Sbjct: 481 MSPTTIVTDPMQQKIMTFMPVIFTVFFLWFPSGLVLYYIVSNLVTIIQQQLIYRGLEKRGL 540

Query: 541 HSREKKKS 548
HSREKKKS
Sbjct: 541 HSREKKKS 548

>ref|NP_709495.1| 60 KD inner-membrane protein [Shigella flexneri 2a str. 301]

Length = 531

Score = 1078 bits (2788), Expect = 0.0

Identities = 530/531 (99%), Positives = 530/531 (99%)

Query: 18 MIWQAWEQDKNPQPQAQQTQTQTTTTAAGSAADQGV PASGQGKLISVKTDVLDLTINTRGG 77
MIWQAWEQDKNPQPQAQQTQTQTTTTAAGSAADQGV PASGQGKLISVKTDVLDLTINTRGG
Sbjct: 1 MIWQAWEQDKNPQPQAQQTQTQTTTTAAGSAADQGV PASGQGKLISVKTDVLDLTINTRGG 60

Query: 78 DVEQALLPAYPKELNSTQPFQLETSPQFIYQAQSGLTGRDGPDPNPANGPRPLYNVEKDA 137
DVEQALLPAYPKELNSTQPFQLETSPQFIYQAQSGLTGRDGPDPNPANGPRPLYNVEKDA
Sbjct: 61 DVEQALLPAYPKELNSTQPFQLETSPQFIYQAQSGLTGRDGPDPNPANGPRPLYNVEKDA 120

Query: 138 YVLAEGQNELQVPMTYTDAAGNTFTKTFVLKRGDYAVNVNYNVQNAGEKPLEISSFGQLK 197
YVLAEGQNELQVPMTYTDAAGNTFTKTFVLKRGDYAVNVNYNVQNAGEKPLEISSFGQLK
Sbjct: 121 YVLAEGQNELQVPMTYTDAAGNTFTKTFVLKRGDYAVNVNYNVQNAGEKPLEISSFGQLK 180

Query: 198 QSITLPPHLD TGSSNFALHTFRGAAYSTPDEKYEKYKFDTIADNENLNIS SKGGWVAMLO 257
QSITLPPHLD TGSSNFALHTFRGAAYSTPDEKYEKYKFDTIADNENLNIS SKGGWVAMLO
Sbjct: 181 QSITLPPHLD TGSSNFALHTFRGAAYSTPDEKYEKYKFDTIADNENLNIS SKGGWVAMLO 240

Query: 258 QYFATAWIPHNDGTNNFYTANLGNIAAIGYKSQPVLVQPGQTGAMNSTLWVGPEIQDKM 317
QYFATAWIPHNDGTNNFYTANLGNIAAIGYKSQPVLVQPGQTGAMNSTLWVGPEIQDKM
Sbjct: 241 QYFATAWIPHNDGTNNFYTANLGNIAAIGYKSQPVLVQPGQTGAMNSTLWVGPEIQDKM 300

Query: 318 AAVAPHLDLTVDYGWLWFISQPLFKLLKWIHSFVGNWGF SIIITFIVRGIMYPLTKAQY 377
AAVAPHLDLTVDYGWLWFISQPLFKLLKWIHSFVGNWGF SIIITFIVRGIMYPLTKAQY
Sbjct: 301 AAVAPHLDLTVDYGWLWFISQPLFKLLKWIHSFVGNWGF SIIITFIVRGIMYPLTKAQY 360

Query: 378 TSMAKMRMLQPKIQAMRERLGDDKQRISQEMMALYKA EKV NPLGGCFPLLIQMPIFLALY 437
TSMAKMRMLQPKIQAMRERLGDDKQRISQEMMALYKA EKV NPLGGCFPLLIQMPIFLALY
Sbjct: 361 TSMAKMRMLQPKIQAMRERLGDDKQRISQEMMALYKA EKV NPLGGCFPLLIQMPIFLALY 420

Query: 438 YMLMG SVELRQAPFALWIHDL SAQDPYYILPILMGVTMFFIQKMSPTTVTDPMQOKIMTF 497
YMLMG SVELRQAPFALWIHDL SAQDPYYILPILMGVTMFFIQKMSPTTVTDPMQOKIMTF
Sbjct: 421 YMLMG SVELRQAPFALWIHDL SAQDPYYILPILMGVTMFFIQKMSPTTVTDPMQOKIMTF 480

Query: 498 MPVIFTVF FFLWFPSGLVLVYYIVSNLV TIIQQQLIYRGLEKRLHSREKKKS 548
MPVIFTVF FFLWFPSGLVLVYYIVSNLV TIIQQQLIYRGLEKRLHSREKKKS
Sbjct: 481 MPVIFTVF FFLWFPSGLVLVYYIVSNLV TIIQQQLIYRGLEKRLHSREKKKS 531

>ref|NP_462742.1| putative preprotein translocase subunit [Salmonella typhimurium
LT2]

Length = 548

Score = 1072 bits (2772), Expect = 0.0

Identities = 522/548 (95%), Positives = 537/548 (97%)

Query: 1 MDSQRNLLVIALLFVSMI WQAWEQDKNPQPQAQQTQTQTTTTAAGSAADQGV PASGQGKL 60
MDSQRNLLVIALLFVSMI WQAWEQDKNPQPQAQQTQTQTTTTAAGSAADQGV PASGQGK+
Sbjct: 1 MDSQRNLLVIALLFVSMI WQAWEQDKNPQPQAQQTQTQTTTTAAGSAADQGV PASGQGKM 60

Query: 61 ISVKTDVLDLTINTRGGDVEQALLPAYPKELNSTQPFQLETSPQFIYQAQSGLTGRDGP 120
I+VKTDVLDLTINTRGGDVEQALLPAYPKEL S +PFQLET+PQFIYQAQSGLTGRDGP
Sbjct: 61 ITVKTDVLDLTINTRGGDVEQALLPAYPKELGSNEPFQLETTTPQFIYQAQSGLTGRDGP 120

Query: 121 DNPANGPRPLYNVEKDAYVLAEGQNELQVPMTYTDAAGNTFTKTFVLKRGDYAVNVNYNV 180
DNPANGPRPLYNVEK+A+VLA+GQNELQVPMTYTDAAGNTFTKTFV KRGDYAVNVNY+V

Sbjct: 121 DNPANGPRPLYNVEKEAFVLADGQNELQVPMTYTDAGNTFTKTFVFKRGDYAVNVNYSV 180

Query: 181 QNAGEKPLEISSFGQLKQSITLPPHLDTGSSNFALHTFRGAAYSTPDEKEYEKYKFDTIAD 240
 QNAGEKPLE+S+FGQLKQS+ LPPH DTGSSNFALHTFRGAAYSTPDEKEYEKYKFDTIAD

Sbjct: 181 QNAGEKPLEVSTFGQLKQSVNLPPHRDTGSSNFALHTFRGAAYSTPDEKEYEKYKFDTIAD 240

Query: 241 NENLNISSEKGGWVAMLQQYFATAWIPHNDDGTNNFYTANLNGIAAIGYKSQPVLVQPGQT 300
 NENLN+SSKGGWVAMLQQYFATAWIP NDGTNNFYTANLNGI AIGYK+QPVLVQPGQT

Sbjct: 241 NENLNVSSKGGWVAMLQQYFATAWIPRNDGTNNFYTANLNGIIVAIGYKAQPVLVQPGQT 300

Query: 301 GAMNSTLWVGPEIQDKMAAVAPHLDLTVDYGWLWFISQPLFKLLKWIHSFVGNWGFSSIII 360
 GAM STLWVGPEIQDKMAAVAPHLDLTVDYGWLWFISQPLFKLLKWIHSFVGNWGFSSIII

Sbjct: 301 GAMSTLWVGPEIQDKMAAVAPHLDLTVDYGWLWFISQPLFKLLKWIHSFVGNWGFSSIII 360

Query: 361 ITFIVRGIMYPLTKAQYTSMAKMRMLQPKIQAMRERLGDDKQRISQEMMALYKAEKVNPL 420
 ITFIVRGIMYPLTKAQYTSMAKMRMLQPKIQAMRERLGDDKQR SQEMMALYKAEKVNPL

Sbjct: 361 ITFIVRGIMYPLTKAQYTSMAKMRMLQPKIQAMRERLGDDKQRQSQEMMALYKAEKVNPL 420

Query: 421 GGCFLPIIQMPIFLALYYMLMGSLVLRQAPFALWIHDLAQDPYYILPILMGVTMFFIQK 480
 GGCFLPI+IQMPIFLALYYMLMGSLVLRQAPFALWIHDLAQDPYYILPILMGVTMFFIQK

Sbjct: 421 GGCFLPIIQMPIFLALYYMLMGSLVLRQAPFALWIHDLAQDPYYILPILMGVTMFFIQK 480

Query: 481 MSPTTVDTPMQQKIMTFMPVIFTVFFLWFPSGLVLYYIVSNLVTIIQQQLIYRGLEKRG 540
 MSPTTVDTPMQQKIMTFMPVIFTVFFLWFPSGLVLYYIVSNLVTIIQQQLIYRGLEKRG

Sbjct: 481 MSPTTVDTPMQQKIMTFMPVIFTVFFLWFPSGLVLYYIVSNLVTIIQQQLIYRGLEKRG 540

Query: 541 HSREKKKS 548
 HSREKKKS

Sbjct: 541 HSREKKKS 548

>ref|NP_458101.1| putative membrane protein [Salmonella enterica subsp. enterica
 serovar Typhi str. CT18]
 ref|NP_807314.1| putative membrane protein [Salmonella enterica subsp. enterica
 serovar Typhi Ty2]
 Length = 548

Score = 1070 bits (2766), Expect = 0.0

Identities = 521/548 (95%), Positives = 535/548 (97%)

Query: 1 MDSQRNLLVIALLFVSFMIWQAWAQDKNPQPQAQQTQTQTTTTAAGSAADQGVASGQGKL 60
 MDSQRNLLVIALLFVSFMIWQAWAQDKNPQPQ QQT QTTTTAAGSAADQGVASGQGK+

Sbjct: 1 MDSQRNLLVIALLFVSFMIWQAWAQDKNPQPQTQQTMTTTTAAGSAADQGVASGQGKM 60

Query: 61 ISVKTVDVLDLTINTRGGDVEQALLPAYPKELNSTQPFQLLETSPQFIYQAQSGLTGRDGP 120
 I+VKTVDVLDLTINTRGGDVEQALLPAYPKEL S +PFQLLET+PQFIYQAQSGLTGRDGP

Sbjct: 61 ITVKTVDVLDLTINTRGGDVEQALLPAYPKELGSNEPFQLLETTPQFIYQAQSGLTGRDGP 120

Query: 121 DNPANGPRPLYNVEKDAYVLAEGQNELQVPMTYTDAGNTFTKTFVLKRGDYAVNVNINV 180
 DNPANGPRPLYNVEKDA+VLA+GQNELQVPMTYTDAGNTFTKTFV KRGDYAVNVNY+V

Sbjct: 121 DNPANGPRPLYNVEKDAFVLADGQNELQVPMTYTDAGNTFTKTFVFKRGDYAVNVNYSV 180

Query: 181 QNAGEKPLEISSFGQLKQSITLPPHLDTGSSNFALHTFRGAAYSTPDEKEYEKYKFDTIAD 240
 QN GEKPLE+S+FGQLKQS+ LPPH DTGSSNFALHTFRGAAYSTPDEKEYEKYKFDTIAD

Sbjct: 181 QNTGEKPLEVSTFGQLKQSVNLPPHRDTGSSNFALHTFRGAAYSTPDEKEYEKYKFDTIAD 240

Query: 241 NENLNISSEKGGWVAMLQQYFATAWIPHNDDGTNNFYTANLNGIAAIGYKSQPVLVQPGQT 300
 NENLN+SSKGGWVAMLQQYFATAWIP NDGTNNFYTANLNGI AIGYK+QPVLVQPGQT

Sbjct: 241 NENLNVSSKGGWVAMLQQYFATAWIPRNDGTNNFYTANLNGIIVAIGYKAQPVLVQPGQT 300

Query: 301 GAMNSTLWVGPEIQDKMAAVAPHLDLTVDYGWLWFISQPLFKLLKWIHSFVGNWGFSSIII 360
 GAM STLWVGPEIQDKMAAVAPHLDLTVDYGWLWFISQPLFKLLKWIHSFVGNWGFSSIII
 Sbjct: 301 GAMSTLWVGPEIQDKMAAVAPHLDLTVDYGWLWFISQPLFKLLKWIHSFVGNWGFSSIII 360

Query: 361 ITFIVRGIMYPLTKAQYTSMAKMRMLQPKIQAMRERLGDDKQRI SQEMMALYKAEKVNPL 420
 ITFIVRGIMYPLTKAQYTSMAKMRMLQPKIQAMRERLGDDKQR SQEMMALYKAEKVNPL
 Sbjct: 361 ITFIVRGIMYPLTKAQYTSMAKMRMLQPKIQAMRERLGDDKQRQSQEMMALYKAEKVNPL 420

Query: 421 GGCFLPIIQMPIFLALYYMLMGSVELRQAPFALWIHDLA QDPYYILPILMGVTMFFIQK 480
 GGCFLPI+IQMPIFLALYYMLMGS+ELR APFALWIHDLA QDPYYILPILMGVTMFFIQK
 Sbjct: 421 GGCFLPIIQMPIFLALYYMLMGSIELRHAPFALWIHDLA QDPYYILPILMGVTMFFIQK 480

Query: 481 MSPTTVTDPMQQKIMTFMPVIFTVFLLWFPSGLVLYYIVSNLVTIIQQQLIYRGLEKRGRL 540
 MSPTTVTDPMQQKIMTFMPVIFTVFLLWFPSGLVLYYIVSNLVTIIQQQLIYRGLEKRGRL
 Sbjct: 481 MSPTTVTDPMQQKIMTFMPVIFTVFLLWFPSGLVLYYIVSNLVTIIQQQLIYRGLEKRGRL 540

Query: 541 HSREKKKS 548
 HSREKKKS
 Sbjct: 541 HSREKKKS 548

>ref|NP_407523.1| probable membrane protein [Yersinia pestis CO92]
 ref|NP_995271.1| probable membrane protein [Yersinia pestis biovar Medievalis str.
 91001]
 ref|NP_671407.1| 60 kDa inner-membrane protein [Yersinia pestis KIM]
 ref|YP_072423.1| Oxal family transporter [Yersinia pseudotuberculosis IP 32953]
 Length = 546

Score = 877 bits (2265), Expect = 0.0

Identities = 423/547 (77%), Positives = 482/547 (88%), Gaps = 1/547 (0%)

Query: 1 MDSQRNLLVIALLFVSMIWAWEQDKNPQQAQQTQTQTTTTAAGSAADQGPASGQGKL 60
 MDSQRNLL+IALLFVSMIWAQW+ D NPQP AQ T QTT TA G A Q VP SGQG+L
 Sbjct: 1 MDSQRNLLVIALLFVSMIWAQWQVDNPNQPTAQTTQTTTNTATGDKASQAVPGSGQGQL 60

Query: 61 ISVKTDVLDLTINTRGGDVEQALLPAYPKELNSTQPFQLETS PQFIYQAQSGLTGRDGP 120
 I+VKTDVL LTINTRGGD+EQA L AYP L S+ F+LLET+P F+YQAQSGLTG++GP
 Sbjct: 61 ITVKTDVLSLTINTRGGDIEQANLLAYPDTLGSSNTFELLETPSFVYQAQSGLTGKNGP 120

Query: 121 DNPANGPRPLYNVEKDAYVLAEGQNELQVPMYTDAGNTFTKTFVLKRGDYAVNVNINV 180
 DNPANG RPL+ V + ++VLA+GQ+EL++P+T+T G+ F KTFVLKR DYA+ V+Y+V
 Sbjct: 121 DNPANGDRPLFEVPQTSFVLADGQDELRIPLTFTSKDGSVFIKTFVLKRNDYAIGVDYHV 180

Query: 181 QNAGEKPLEISSFGQLKQSITLPPHLDTGSSNFALHTFRGAAYSTPDEKYEKFKFTDIAD 240
 NA PLE++ FGQLKQSI LP DTGS+NFAL T+RGAAYS+ + KY+KY F I D
 Sbjct: 181 NNASAAPLELTLFGQLKQSINLPKKRDTGSNNFALQTYRGAAYSSDETKYKKYSFSDIED 240

Query: 241 NENLNISCKGGWVAMLQQYFATAWIPHN DGTNNFYTANLGNGIAAIGYKSQPVLVQPGQT 300
 +NL+I++KGGWVAMLQQYFATAWIP + TN FY+A LGNG+AAIG+K PV++QPG+
 Sbjct: 241 -KNLDITTKGGWVAMLQQYFATAWIPAA NETNTFYSAELGNGLAAIGFKGAPVVIQPGEQ 299

Query: 301 GAMNSTLWVGPEIQDKMAAVAPHLDLTVDYGWLWFISQPLFKLLKWIHSFVGNWGFSSIII 360
 +++TLWVGPEIQ+KMA +APHLDLTVDYGWLWFISQPLFKLLK+IHSFVGNWGFSSII+
 Sbjct: 300 KQLSATLWVGPEIQNKMAEIAPHLDLTVDYGWLWFISQPLFKLLKFIHSFVGNWGFSSIIIV 359

Query: 361 ITFIVRGIMYPLTKAQYTSMAKMRMLQPKIQAMRERLGDDKQRI SQEMMALYKAEKVNPL 420
 ITFIVRGIMYPLTKAQYTSMAKMR+LQPK+ AMRER+GDDKQR+SQEMMALYKAEKVNPL
 Sbjct: 360 ITFIVRGIMYPLTKAQYTSMAKMRLLQPKLAAMRERIGDDKQRMSQEMMALYKAEKVNPL 419

Query: 421 GGC FPLLIQMPIFLALYYMLMG SVELRQAPFALWIHDLSAQDPYYILPILMGVTMFFIQK 480
 GGC PL+IQMPIFLALYYMLM SVELR APF LWIHDLSAQDPYYILPILMG+TM+FIQK
 Sbjct: 420 GGCLPLIIQMPIFLALYYMLMSSVELRHAPFILWIHDLSAQDPYYILPILMGITMYFIQK 479

Query: 481 MSPTTVTDPMQQKIMTFMPVIFTVFFLWFP SGLVLYYIVSNLVTIIQQQLIYRGLEKRGL 540
 MSPTTVTDPMQQKIMTFMPVIFTVFFLWFP+GLVLYYIVSNLVTI+QQQLIYRGLEKRGL
 Sbjct: 480 MSPTTVTDPMQQKIMTFMPVIFTVFFLWFPAGLVLYYIVSNLVTIILQQQLIYRGLEKRGL 539

Query: 541 HSREKKK 547
 HSREKKK
 Sbjct: 540 HSREKKK 546

>ref|NP_932057.1| hypothetical protein [Photorhabdus luminescens subsp. laumondii
 TTO1]
 Length = 546

Score = 850 bits (2196), Expect = 0.0
 Identities = 410/546 (75%), Positives = 471/546 (86%), Gaps = 3/546 (0%)

Query: 1 MDSQRNLLVIALLFVSFMIWQAWEQDKNPQPQAQQTQTQTTTAAAGSAADQGV PASGQGKL 60
 MDSQRNLL+IALLFVSF++WQAW E DKNPQP Q TQ T S+ +Q VP SG+GKL
 Sbjct: 1 MDSQRNLLVIALLFVSFVLVWQAW EADKNPQPTTVQATQQTDMPP--SSENQAVPGSGKGKL 58

Query: 61 ISVKTDVLDLTINTRGGDVEQALLPAYPKELNSTQPFQ LLETSPQFIYQAQSGLTGRDGP 120
 I+VKTDVL LTINTRGGD+E+A L AYP L S QPF+LLET+P F YQAQSGLTG+DGP
 Sbjct: 59 ITVKTDVLSLTINTRGGDIEEADLLAYPDTLGSNQPFKLLETTPAFTYQAQSGLTGKDGP 118

Query: 121 DNPANGPRPLYNVEKDAYVLAEGQNELQVPMTYTDAAGNTFTKTFVLKRGDYAVNVNINV 180
 DNP N RPLY +D+YVLA+GQ+EL++PM + G + KTFVLKRG+YA++V+Y +
 Sbjct: 119 DNP MNSERPLYTAAQDSYVLADGQDELRI PMNFVTKNGIVYVKT FVLKRGEY AISVDYRI 178

Query: 181 QNAGEKPLEISSFGQLKQSITLPPHLD TGSSNFALHTFRGAAYSTPDEKYEKYKFDTIAD 240
 N EKPL+++ FGQLKQS+ LP H DTGSSNFALHT+RGAAYS+ D KY+KY F I +
 Sbjct: 179 HNTTEKPLQMTFFGQLKQSVELPKHRDTGSSNFALHTYRGAAYSSDDTKYKKYSFSDI-E 237

Query: 241 NENLNIS SKGGWVAMLQQYFATAWI PHNDGTNNFY TANLNGIAAIGYKSQPVLVQPGQT 300
 E+L++++KGGW+AMLQQYFATAW+P + T+ FYT LG +AAIGYKS P+ V
 Sbjct: 238 GESLSVTTKGGWIAMLQQYFATAWVPVANETSTFYTVALGKEMAAIGYKSAPISVAANSE 297

Query: 301 GAMNSTLWVGPEIQDKMAAVAPHLDLTV DYGWLWFISQPLFKLLKWIHSFVGNWGF SIII 360
 ++STLW+GPEIQD+MAAVAPHLDL+VDYGWLWFISQPLFKLLK++H F+GNWGF SII+
 Sbjct: 298 KTVSSTLWIGPEIQDEMAAVAPHLDLSDYGWLWFISQPLFKLLKFLHGFIGNWGF SIIIV 357

Query: 361 ITFIVRGIMYPLTKAQYTSMAKMRMLQPKIQAMRERLGDDKQRISQEMMALYKA EKV NPL 420
 ITFIVRGIMYPLTKAQYTSMAKMR+LQPK+ AMRER+GDDKQR+SQEMMALYKA EKV NPL
 Sbjct: 358 ITFIVRGIMYPLTKAQYTSMAKMRLLQPKLAAMRERIGDDKQRMSQEMMALYKA EKV NPL 417

Query: 421 GGC FPLLIQMPIFLALYYMLMG SVELRQAPFALWIHDLSAQDPYYILPILMGVTMFFIQK 480
 GGC PLIIQMPIFLALYYMLMG SVELR APFA WIHDLSAQDPYYILP+LMGV TMF IQK
 Sbjct: 418 GGCLPLIIQMPIFLALYYMLMG SVELRHAPFAGWIHDLSAQDPYYILPLL MGVTMFI IQK 477

Query: 481 MSPTTVTDPMQQKIMTFMPVIFTVFFLWFP SGLVLYYIVSNLVTIIQQQLIYRGLEKRGL 540
 MSPTT+TDPMQQKIMT+MPVIFT+FFLWFP SGLVLYYIVSNLVTIIQQQLIYRGLEKRGL
 Sbjct: 478 MSPTTITDPMQQKIMTYMPVIFTIFFLWFP SGLVLYYIVSNLVTIIQQQLIYRGLEKRGL 537

Query: 541 HSREKK 546
 HSREKK

Sbjct: 538 HSREKK 543

>ref|NP_239857.1| 60 kDa inner-membrane protein [Buchnera aphidicola str. APS
(Acyrtosiphon pisum)]
Length = 532

Score = 642 bits (1657), Expect = 0.0

Identities = 315/538 (58%), Positives = 392/538 (72%), Gaps = 9/538 (1%)

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Query: 1  MDSQRNLLVIALLFVSFMIWQAWAQDKNPQPQAQQTQTQTTTTAAGSAADQGVPPASGQGKL 60
      M+ QRN + A LFVSF++WQAW          Q+Q          T          +          K
Sbjct: 1  MEVQRNFFIFAF LFVSFLLWQAW-----QSQMFLNKKKTNEKIDPIFHFIDVKKNNKKK 52

Query: 61  ISVKTVDVLDLTINTRGGDVEQALLPAYPKELNSTQPFQLETSPPQFIYQAQSGLTGRDGP 120
      I +K DV+ L +N GGDVE+A L AY   L S++PF+LLET   FIYQAQSGL G+DGP
Sbjct: 53  IFIKNDVISLVNMYGGDVEEASLLAYKDTLYSSRPFKLLETGSDFIYQAQSGLIGKDGP 112

Query: 121  DNPANGPRPLYNVEKDAYVLAEGQNELQVPMYTDAGNTFTKTFVLKRGDYAVNVNINV 180
      D+  N RPLY+ K+ +VL  + EL+VP+ +   G  + KTF+LK   Y V + Y+V
Sbjct: 113  DSSINDSRPLYSANKNFFVLGPNEKELRVPIKWLKNGVVIYKKTFILKPNRYDVQIEYDV 172

Query: 181  QNAGEKPLEISSFGQLKQSITLPPHLDTGSSNFALHTFRGAAYSTPDEKEYEKYKFDTIAD 240
      N ++ L ++ FGQ+KQ+I LP   + S NFAL TFRGAAYS+ D KYEKYKFD IA+
Sbjct: 173  YNPSKESLNMNIFGQIKQTINLPKKNRVYSGNFALQTFRGAAYSSDDNKYEKYKFDMIAN 232

Query: 241  NENLNISSKGGWVAMLQQYFATAWIPHN DGTNNFYTANLGNIAAIGYKSQPVLVQPGQT 300
      N+NL+I ++ GW+AMLQQYFA AWIP N G N  YT++L +  A IGYKS  + + P
Sbjct: 233  NKNLHIMTESGWIAMLQQYFAVAWIPDNLGKNTIYTSSLDHTAVIGYKSPIINIPPNSR 292

Query: 301  GAMNSTLWVGPEIQDKMAAVAPHLDLTVDYGWLWLFISQPLFKLLKWIHSFVGNWGFSSII 360
      + S LW+GP+IQ +M  VAP+LDLTVDYGWLWF+SQPLFKLL  ++S +GNWGFSSII+
Sbjct: 293  SIIKSLWIGPKIQKEMKLVAPNLDLTVDYGWLWFLSQPLFKLLTILYSIIGNWGFSSII 352

Query: 361  ITFIVRGIMYPLTKAQYTSMAKMRMLQPKIQAMRERLGDDKQRISQEMMALYKAEKVNPL 420
      ITFI+RG+ YPLTKAQY SMAKMR LQPKIQ ++E+   DKQRISQEM+ LYK EK+NPL
Sbjct: 353  ITFIMRGLTYPLTKAQYISMAKMRALQPKIQEIKEKFSKDKQRISQEMILLYKKEKINPL 412

Query: 421  GGCFLPII QMPIFLALYYMLMGVSVELRQAPFALWIHDL SAQDPYYILPILMGVTMFFIQK 480
      GG  P+ IQMPIFL+LYYML+GSVELR APF LWIHDL S+QDPYY+LP++MG+TMFFIQK
Sbjct: 413  GGFLPIFIQMPIFLSLYYMLIGSVELRHAPFLWIIHDLSSQDPYYVLPVIMGLTMFFIQK 472

Query: 481  MSPTT-VTDPMQQKIMTFMPVIFTVFFLWFPSGLVLYYIVSNLVTIIQQQLIYRGLEK 537
      +S T  ++DP+Q+KIM FMPVIFT FFLWFPSGLVLYYI+SNLVTIIQQ+ I  LEK
Sbjct: 473  ISSTNHISDPLQKKIMNFMFVIFTAFFLWFPSGLVLYYIISNLVTIIQQKFILSNLEK 530

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>ref|NP_796382.1| inner membrane protein, 60 kDa [Vibrio parahaemolyticus RIMD
2210633]
Length = 540

Score = 622 bits (1605), Expect = e-177

Identities = 322/549 (58%), Positives = 406/549 (73%), Gaps = 15/549 (2%)

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Query: 1  MDSQRNLLVIALLFVSFMIWQAWAQDKNPQPQAQQTQTQTTTTA-AGSAADQGVPPASGQ-- 57
      MDSQRN+L+IAL VSF+++Q W+  KNP PQA +  Q++++  A S AD+  P  GQ
Sbjct: 1  MDSQRNILLIALALVSFLLFQQWQVAKNPAPQAVEQAQSSSLPAPSFADLDPVPGQQQ 60

```

Query: 58 --GKLISVKTDVLDLTINTRGGDVEQALLPAYPKELNSTQPFQLETSPQFIYQAQSGLT 115
 K I+V TDVL L+I+T GGDV A L Y EL+S+ PF LL+ + + AQSGL
 Sbjct: 61 ASAKTITVTTDVLTLSIDTVGGDVVHADLNQYSAELDSSDPFVLLKDTQGHQFIAQSGLV 120

Query: 116 GRDGPDPNPANGPRPLYNVEKDAYVLAEGQNELQVPMTYTDAGNTFTKTFVLKRGDYAVN 175
 G G D ++ RP YNV D++ LA+GQ+EL+VPMT+T A G +TKT+VLKRG YA+N
 Sbjct: 121 GPQGIDLSSSN-RPHYNVSADSFTLADGQDELRVPMFT-ANGIEYTKTYVLKRGSYALN 178

Query: 176 VNYNVQNAGEKPLEISSFGQLKQSITLPPHLDTGSSNFALHTFRGAAYSTPDEKYEKYKF 235
 V Y+V N + L+Q++ +D G S + T+RG AYST D +Y+KY F
 Sbjct: 179 VEYDVANNSGNNATFGMYAHLRQNL-----MDAGGS-ITMPTYRGGAYSTEDTRYKKYSF 232

Query: 236 DTIAD-NENLNISSEKGGWVAMLQQYFATAWIPHNDGTNNFYTANLGNIAAIGYKSQPV 294
 + + D N ++N++ GW AM+Q YFA AWIP N+ N YT +GN + IG +
 Sbjct: 233 EDMQDRNLSINLADGQGWAAMIQHYFAAAWIPRNEPGTNLYTRVIGN-LGDIGVRMPNKT 291

Query: 295 VQPGQTGAMNSTLWVGPEIQDKMAAVAPHLDTVDYGWLWFIQSPLFKLLKWIHSFVGNW 354
 + G +TLWVGP++Q +MAAVAP+LDL VDYGWLWFI++PL LL +I SFVGNW
 Sbjct: 292 IATGDQAKFEATLWVGPKLQQEMAAPNLDLVVDYGWLWFIKPLHSLLAFIQS FVGNW 351

Query: 355 GFSIIITFIVRGIMYPLTKAQYTSMAKMRMLQPKIQAMRERLGDDKQRISQEMMALYKA 414
 G +II +TFIVRG MYPLTKAQYTSMAKMRMLQPK+QAMRER+GDD+QR+SQEMM LYK
 Sbjct: 352 GVAIIICLT FIVRGAMYPLTKAQYTSMAKMRMLQPKLQAMRERIGDDRQRMSQEMMELYKK 411

Query: 415 EKNVPLGGCFPLLIQMPIFLALYYMLMGVELRQAPFALWIHDLAQDPYYILPILMGVT 474
 EKNVPLGGC PL++QMPIF+ALY+ LM SVELR +PF WIHDLAQDPYYILP+LMG +
 Sbjct: 412 EKNVPLGGCLPLVLQMPIFIALYWALMESVELRHSPPFGWIHDLAQDPYYILPLLMGAS 471

Query: 475 MFFIQKMSPTTVTDPMQKIMTFMPVIFTVFFLWFPGLVLYYIVSNLVTIIQQQLIYRG 534
 MF IQKMSPTTVTDPMQKIMTFMPV+FT FFL+FPSGLVLY++VSN+VT+IQQ LIY+
 Sbjct: 472 MFLIQKMSPTTVTDPMQKIMTFMPVMFTFFFLFFPSGLVLYWLVSNIIVTLIQTTLIYKA 531

Query: 535 LEKRGLHSR 543
 LEK+GLH++
 Sbjct: 532 LEKKGLHTK 540

>ref|NP_932796.1| inner membrane protein, 60 kDa [Vibrio vulnificus YJ016]
 Length = 539

Score = 620 bits (1600), Expect = e-177

Identities = 322/548 (58%), Positives = 401/548 (73%), Gaps = 14/548 (2%)

Query: 1 MDSQRNLLVIALLFVSFMIWQAWEQDKNPQPAQQTQTQTTTTA-AGSAADQGV PASGQ-- 57
 MDSQR LLV+ L VSF+++Q W+ KNP PQA + QT++T A S AD+ PA Q
 Sbjct: 1 MDSQRTLLVLLLALVSFLLFQQWQVAKNPAPQAVEQAQTSSTLPAPSFADLDPAPAQQA 60

Query: 58 -GKLISVKTDVLDLTINTRGGDVEQALLPAYPKELNSTQPFQLETSPQFIYQAQSGLTG 116
 KLI+V TDVL L+I+T GGDV A L Y ELNS F+LL + + AQSGL G
 Sbjct: 61 SAKLITVTTDVLTLSIDTVGGDVVAADLNQYSAELNSANAFELLRDTQGHQFIAQSGLVG 120

Query: 117 RDGPDNPANGPRPLYNVEKDAYVLAEGQNELQVPMTYTDAGNTFTKTFVLKRGDYAVNV 176
 G D +N RP Y V D++ LA+ QNEL++PMTY A G +TKTF+LKRG YA++V
 Sbjct: 121 PQGIDLSSNN-RPSYQVSADSFTLADDQNELRIPTY-QANGLEYTKTFILKRGSYAIDV 178

Query: 177 NYNVQNAGEKPLEISSFGQLKQSITLPPHLDTGSSNFALHTFRGAAYSTPDEKYEKYKFD 236
 ++V N + + L+Q++ +D G S + T+RG AYST D +Y+KY F+
 Sbjct: 179 EFDVINKSGNNATLGMYAHLRQNL-----MDAGGS-ITMPTYRGGAYSTEDTRYKKYSFE 232

Query: 237 TIAD-NENLNISSEKGGWVAMLQQYFATAWIPHNDGTNNFYTANLNGIAAIGYKSQPVLV 295
 + D N +L +++ GW AM+Q YFA AWIP N+ N YT +GN + IG + V
 Sbjct: 233 DMQDRNLSLTLTNGQGWAAMIQHYFAAAWIPRNEPGANLYTRVIGN-MGDIGVRMPNKTV 291

Query: 296 QPGQTGAMNSTLWVGPEIQDKMAAVAPHLDLTVDYGWLWFIQSPLFKLLKWIHSFVGNWG 355
 G + +TLW GP++QD+MA VAP+LDL VDYGWLWFI++PL LL I SFVGNWG
 Sbjct: 292 ADGDSAHTATLWAGPKLQDQMAEVAPNLDLVVDYGWLWFIKPLHWLLSVIQSFVGNWG 351

Query: 356 FSIIITFIVRGIMYPLTKAQYTSMAKMRMLQPKIQAMRERLGDDKQRISQEMMALYKAE 415
 +II +TFIVRG MYPLTKAQYTSMAKMRMLQPK+QAMRER+GDD+QR+SQEMM LYK E
 Sbjct: 352 VAIICLTFIVRGAMYPLTKAQYTSMAKMRMLQPKLQAMRERIGDDRQRMSQEMMELYKKE 411

Query: 416 KVNPLGGCFPLLIQMPIFALYMLMGSVELRQAPFALWIHDLAQDPYYILPILMGVTM 475
 KVNPLGGC PL++QMPIF+ALY+ LM SVELR +PF LWIHDLAQDPY+ILP+LMG +M
 Sbjct: 412 KVNPLGGCLPLILQMPIFIALYWALMESVELRHSPFILWIHDLAQDPYFILPLLMGGSM 471

Query: 476 FFIQKMSPTTVDTPMQQKIMTFMPVIFTVFLLWFPGLVLYYIVSNLVTIIQQQLIYRGL 535
 F IQKMSPTTVDTPMQQKIMTFMPV+FT FFLWFPGLVLY++VSN+VT+IQQ LIY+ L
 Sbjct: 472 FLIQKMSPTTVDTPMQQKIMTFMPVMTFFFLWFPGLVLYWLVSNIIVTLIIQQSLIYKAL 531

Query: 536 EKRGLHSR 543
 EK+GLH++
 Sbjct: 532 EKKGLHTK 539

>ref|NP_759968.1| Inner membrane protein, 60 kDa [Vibrio vulnificus CMCP6]
 Length = 539

Score = 620 bits (1599), Expect = e-177

Identities = 321/548 (58%), Positives = 401/548 (73%), Gaps = 14/548 (2%)

Query: 1 MDSQRNLLVIALLFVSFMIWQAWEQDKNPQQAQQTQTQTTTTA-AGSAADQGV PASGQ-- 57
 MDSQR LLV+ L VSF+++Q W+ KNP PQA + QT++T A S AD+ PA Q
 Sbjct: 1 MDSQRTLLVLLLALVSFLLFQQWQVAKNPAPQAVEQAQTSSTLPAPSFADLDPAPAQQA 60

Query: 58 -GKLISVKTDVLDLTINTRGGDVEQALLPAYPKELNSTQPFQLLETSPQFIYQAQSGLTG 116
 KLI+V TDVL L+I+T GGDV A L Y ELNS F+LL + + AQSG L G
 Sbjct: 61 SAKLITVTTDVLTLSIDTVGGDVVAADLNQYSAELNSANAFELLRDTQGHQFIAQSGLVG 120

Query: 117 RDGPDNPANGPRPLYNVEKDAYVLAEGQNELQVPMTYTDAAGNTFTKTFVLKRGDYAVNV 176
 G D +N RP Y V D++ LA+ QNEL++PMTY A G +TKTF+LKR G YA++V
 Sbjct: 121 PQGIDLSSNN-RPSYQVSADSFTLADDQNELRIPMTY-QANGLEYTKTFILKRGSY AIDV 178

Query: 177 NYNVQNAGEKPLEISSFGQLQSITLPPHLDTGSSNFALHTFRGAAYSTPDEKYEKFKFD 236
 ++V N + + L+Q++ +D G S + T+RG AYST D +Y+KY F+
 Sbjct: 179 EFDVINKSGNNATLGMYAHLRQNL-----MDAGGS-ITMPTYRGAYSTEDTRYKKYSFE 232

Query: 237 TIAD-NENLNISSEKGGWVAMLQQYFATAWIPHNDGTNNFYTANLNGIAAIGYKSQPVLV 295
 + D N +L +++ GW AM+Q YFA AWIP N+ N YT +GN + IG + +
 Sbjct: 233 DMQDRNLSLTLTNGQGWAAMIQHYFAAAWIPRNEPGANLYTRVIGN-MGDIGVRMPNKT I 291

Query: 296 QPGQTGAMNSTLWVGPEIQDKMAAVAPHLDLTVDYGWLWFIQSPLFKLLKWIHSFVGNWG 355
 G + +TLW GP++QD+MA VAP+LDL VDYGWLWFI++PL LL I SFVGNWG
 Sbjct: 292 ADGDSAHTATLWAGPKLQDQMAEVAPNLDLVVDYGWLWFIKPLHWLLSVIQSFVGNWG 351

Query: 356 FSIIITFIVRGIMYPLTKAQYTSMAKMRMLQPKIQAMRERLGDDKQRISQEMMALYKAE 415
 +II +TFIVRG MYPLTKAQYTSMAKMRMLQPK+QAMRER+GDD+QR+SQEMM LYK E
 Sbjct: 352 VAIICLTFIVRGAMYPLTKAQYTSMAKMRMLQPKLQAMRERIGDDRQRMSQEMMELYKKE 411

Query: 416 KVNPLGGCFPLLIQMPIFLALYYMLMGSVELRQAPFALWIHDLSAQDPYYILPILMGVTM 475
 KVNPLGGC PL++QMPIF+ALY+ LM SVELR +PF LWIHDLSAQDPY+ILP+LMG +M
 Sbjct: 412 KVNPLGGCLPLILQMPIFIALYWALMESVELRHSPFILWIHDLSAQDPYFILPLLMGGSM 471

Query: 476 FFIQKMSPTTVDTPMQQKIMTFMPVIFTVFFLWFPSGLVLYYIVSNLVTIIQQQLIYRGL 535
 F IQKMSPTTVDTPMQQKIMTFMPV+FT FFLWFPSGLVLY++VSN+VT+IQQ LIY+ L
 Sbjct: 472 FLIQKMSPTTVDTPMQQKIMTFMPVMFTFFFLWFPSGLVLYWLVSNIIVTLIIQQSLIYKAL 531

Query: 536 EKRGLHSR 543
 EK+GLH++
 Sbjct: 532 EKKGLHTK 539

>ref|NP_660377.1| inner membrane protein [Buchnera aphidicola str. Sg (Schizaphis graminum)]
 Length = 537

Score = 617 bits (1592), Expect = e-176
 Identities = 308/540 (57%), Positives = 386/540 (71%), Gaps = 11/540 (2%)

Query: 1 MDSQRNLLVIALLFVSMIWAWEQDKNPQQAQQTQTTTTAAGSAADQGV PASGQKGL 60
 M+ QRN + A LFVSF++WQAW+ + + + T + D+
 Sbjct: 2 MELQRNFFIFAFLFVSFLLWQAWQSQSLKKNKNEETNSFFHLNHHKEDKNQ----- 53

Query: 61 ISVKTDVLDLTINTRGGDVEQALLPAYPKELNSTQPFQLETSPOFIYQAQSGLTGRDGP 120
 I +K DVL L IN GGD+E+A L Y +LNS + +LLET F+YQAQSGL G+DG
 Sbjct: 54 IIIKNDVLRVLINMYGGDIEEASLLDYKTQLNSPENLKLLETKSDFVYQAQSGLIGKDGL 113

Query: 121 DNPANGPRPLYNVEKDAYVLAEGQNELQVPMTYTDAAGNTFTKTFVLKRGDYAVNVNINV 180
 DN N RPLY+ +K+ + L + EL+VP+T+ G T+ K F+LK G Y V V Y++
 Sbjct: 114 DNSINKIRPLYSAKKNFFELGHNEKELRVPITFIKNGITYIKNFILKPGKYNVEVEYDI 173

Query: 181 QNAGEKPLEISSFGQLKQSITLPPHLDTGSSNFALHTFRGAAYSTPDEKEYEKYKFDTIAD 240
 N K LE++ FGQLKQ++ LP + D S NFAL TFRGAAYS+ D KYEKYKFD IA+
 Sbjct: 174 NNLSNKKLELNIFGQLKQTVKLPKNRDIYSGNFALQTFRGAAYSSSDAKYEKYKFDNIAN 233

Query: 241 NENLNISSKGGWVAMLQQYFATAWIPHND--GTNNFYTANLGN-GIAAIGYKSQPVLVQP 297
 +E+L+I + GW+AMLQQYF AW+P + +N YT+ L N GIA IGYKS + +
 Sbjct: 234 HEHLHIITHHGWIAMLQQYFVVAWVPDTNISSSNIIYTSYLDNDGIAIIGYKSSLINIPS 293

Query: 298 GQTGAMNSTLWVGPEIQDKMAAVAPHLDTVDYGWLWFISQPLFKLLKWIHSFVGNWGF 357
 + S LW+GPE Q +MA VAP+LDLTVDYD+LWF+SQPLFKLL IH+F+GNWGF
 Sbjct: 294 NSRYIIKSKLWIGPEKQEMALVAPNLDLTVDYDGLWFLSQPLFKLLSTIHNFIGNWGF 353

Query: 358 IIIITFIVRGIMYPLTKAQYTSMAKMRMLQPKIQAMRERLGDDKQRISQEMMALYKAKEV 417
 II+ITF+++ I YPLTKAQYTSM+KMR LQPKI +++ G DKQR+S+E+MALYK EK+
 Sbjct: 354 IILITFMMKAITYPLTKAQYTSMSKMRELQPKINELKKNFGHDKQMSKEIMALYKKEKI 413

Query: 418 NPLGGCFPLLIQMPIFLALYYMLMGSVELRQAPFALWIHDLSAQDPYYILPILMGVTMFF 477
 NPLGGC P+ IQMPIFL+LYYML+GSVELR APF WI DLS QDPYY+LPI MG+TMFF
 Sbjct: 414 NPLGGCLPVFIQMPIFLSLYYMLIGSVELRHAPFLFWIKDLSQDPYYVLPIMGLTMFF 473

Query: 478 IQKMSPTTVDTPMQQKIMTFMPVIFTVFFLWFPSGLVLYYIVSNLVTIIQQQLIYRGLEK 537
 IQ+ S ++DP QQKIM FMP IFTVFFLWFPSGLVLYYIVSNLVTIIQQ+ I +K
 Sbjct: 474 IQRSSNNISDPFQQKIMHFMPFIFTVFFLWFPSGLVLYYIVSNLVTIIQQKYILSNFKK 533

>ref|YP_087673.1| YidC protein [Mannheimia succiniciproducens MBEL55E]

Length = 540

Score = 617 bits (1591), Expect = e-176

Identities = 310/551 (56%), Positives = 398/551 (72%), Gaps = 17/551 (3%)

Query: 1 MDSQRNLLVIALLFVSFMIWQAWQDKN-PQPQAQQTQTQTTT-----AAGSAADQGVPA 54
MDS+R+LLV+ALLF+SF++++ W+ D N P+P A + Q ++ A+ S+ + V
Sbjct: 1 MDSRRSLLVLALLFISFLVYEQWQMDYNTPKPVATEQAQAVSSNAEMPASTSSTEGTVDN 60

Query: 55 SGQGKLISVKTDVLDLTINTRGGDVEQALLPAYPKELNSTQPFQLLETSPQFIYQAQSG 114
QGK+IS++ DV L ++T GGDV ++ L Y ELNS F LL+ P +Y AQSG
Sbjct: 61 VAQGKIISIQNDFTLKVDLTGGDVVSSLTNYAAELNSDARFILLQNKPNVEVYVAQSG 120

Query: 115 TGRDGPDPNPANGPRPLYNVEKDAYVLAEGQNELQVPMTYTDAAGNTFTKTFVLKRGDYAV 174
G++G D A R Y VE + + LA+GQNEL+VP+T + G + K FV+K G Y +
Sbjct: 121 IGKNGIDTKAG--RAAYQVEAEQFTLADGQNELRVPLTL-EKDGVIYRKVFVIKAGSYDI 177

Query: 175 NVNYNVQNAGEKPLEISSFGQLKQSITLPPHLDTGSSNFALHTFRGAAYSTPDEKEYEKYK 234
VNY +QN + +E+ +GQLK ++ S + A+ T+ G AYS+ D Y+KY
Sbjct: 178 EVNYEIQNQTNEAIEVQPYGQLKHTLV-----QSSGSMAMPTYTGGAYSSADTNYKKYS 231

Query: 235 FDTIADNENLNISCKGGWVAMLQQYFATAWIPHNDGTNNFYTANLGNIAAIGYKSQPVL 294
FD + D +NL+I +K GWVA+LQ YF +AWIP+ D N YT+ NG+ IGY+ V
Sbjct: 232 FDEMKD-KNLSIDTKAGWVAVLQHYFVSAWIPNQDADNQLYTST-ANGLGFIGYRGPV 289

Query: 295 VQPGQTGAMNSTLWVGPEIQDKMAAVAPHLDTVDYGLWLFISQPLFKLLKWIHSFVGNW 354
V G + + S LW GP++Q++M AVA HLDLTVDYGW WFI++PLF LL I S V NW
Sbjct: 290 VPAGGSETIKSALWTGPKLQNMGAHANHLDTVDYGWAWFIAKPLFWLLNVIQSI 349

Query: 355 GFSIIITFIVRGIMYPLTKAQYTSMAKMRMLQPKIQAMRERLGDDKQRISQEMMALYKA 414
G +II +T +V+GI+YPLTKAQYTSMAKMRMLQPK+Q MRER GDD+QR+SQEMM LYK
Sbjct: 350 GLAIIGVTIVVKGILYPLTKAQYTSMAKMRMLQPKLQEMRERFGDDRQRMSQEMMKLYKE 409

Query: 415 EKVNPGLGGCFPLLIQMPIFLALYMLMGVSLRQAPFALWIHDLAQDPYYILPILMGVT 474
EKVNPLGGC PLLIQMPIF+ALY+ M +VELR APF WI DLSAQDPYYILPILMG +
Sbjct: 410 EKVNPGLGGCLPLLIQMPIFIALYWTFMEAVELRHAPFFGWIQDLSAQDPYYILPILMGAS 469

Query: 475 MFFIQKMSPTTVDPMQKIMTFMPVIFTVFFLWFPGLVLYYIVSNLVTIIQQQLIYRG 534
MF +QKMSPT V DPMQKIM FMP+IF VFFLWFP+GLVLY++VSN++TI+QQQLIYRG
Sbjct: 470 MFLQKMSPTPVADPMQKIMNFMPLIFMVFFLWFPAGLVLYWLVSNIITIVQQQLIYRG 529

Query: 535 LEKRGHLSREK 545
LEK+GLHSR+K
Sbjct: 530 LEKKGHLSRKK 540

>ref|NP_062588.1| inner membrane protein, 60 kDa [Vibrio cholerae O1 biovar eltor
str. N16961]
Length = 541

Score = 614 bits (1583), Expect = e-175

Identities = 320/553 (57%), Positives = 402/553 (72%), Gaps = 22/553 (3%)

Query: 1 MDSQRNLLVIALLFVSFMIWQAWQDKNPQPQAQQTQTQTTTAA-AGSAADQGVPA 58
MDSQRN+L+IAL VSF+++Q W+ KNP PQA Q Q+T A A S +D+ P Q
Sbjct: 1 MDSQRNILLIALALVSFLFQWQVAKNPAPQATQQAQSTGAAPAPSFSELDPTPAQNV 60

Query: 59 ----KLISVKTDVLDLTINTRGGDVEQALLPAYPKELNSTQPFQLLETSPQFIYQAQSG 114
K I+V TDVL L+I+T GGDV A L Y +ELNS + F LL+ + + AQSG

Sbjct: 61 AAKAKTITVSTDVLTLSIDTLGGDVVS AKLNQYSEELNSPESFVLLQNTQGHQFIAQSGL 120

Query: 115 TGRDGPDPNANGPRPLYNVEKDAYVLAEGQNELQVPMTYTDAGNTFTKTFVLKRGDYAV 174
 G G D +N RP Y V D++ LAEGQ+EL++PMTY A G +TKTF+LKR G YAV

Sbjct: 121 VGPQGIDVTSNN-RPAYQVSADSFTLAEGQDELRIPTY-QANGIDYTKTFILKRGSYAV 178

Query: 175 NVNYNVQNAGEKPLEISSFGQLKQSITLPPHLDTGSSNFALHTFRGAAYSTPDEKEYEKYK 234
 +V ++V N + + L+Q++ LD+G N A+ T+RG AYST D +Y+KY

Sbjct: 179 DVVFDVANNSGSEATLGMZYAHLRQNL-----LDSSG-NLAMPTYRGGAYSTSDVRYKKYS 232

Query: 235 FDTIADNENLNISSEK-----GWVAMLQQYFATAWIPHNDGTNNFYTANLNGIAAIGYKS 290
 FD + D N+S+ WVAM+Q YFA+AWIP ++ Y+ + N + +G ++

Sbjct: 233 FDDMKDR---NLSAPNDVTVNWVAMIQHYFASAWIPRDEPQAQLYSRVINN-LGDMGIRT 288

Query: 291 QPVLVQPGQTGAMNSTLWVGPEIQDKMAAVAPHLDLTVDYGWLWFIQPLFKLLKWIHSF 350
 + G +TLWVGP++QD+MAA AP+LDL VDYGWLWFI++PL LL I +F

Sbjct: 289 PNKTIANGDKAEFEATLWVGPKLQDQMAATAPNLDLVVDYGWLWFIKPLHWLLSVIQT 348

Query: 351 VGNWGFSSIIITFIVRGIMYPLTKAQYTSMAKMRMLQPKIQAMRERLGDDKQRISQEMMA 410
 VGNWG +II +TFIVRG MYPLTKAQYTSMAKMRMLQPK+QAMRER+GDD+QR+SQEMM

Sbjct: 349 VGNWGVAIICLTFIVRGAMYPLTKAQYTSMAKMRMLQPKLQAMRERIGDDRQRMSQEMME 408

Query: 411 LYKAEKVNPLGGCFPLLIQMPIFLALYYMLMGSSVELRQAPFALWIHDLAQDPYYILPIL 470
 LYK EKNVPLGGC P+L+QMPIF+ALY+ LM SVELR +PF WIHDLAQDPYYILP+L

Sbjct: 409 LYKKEKVNPLGGCLPILLQMPIFIALYWALMESVELRHSPPFGWIHDLAQDPYYILPLL 468

Query: 471 MGVTMFFIQKMSPTTVDPMQQKIMTFMPVIFTVFFLWFPSGLVLYYIVSNLVTIIQQQL 530
 MG +MF IQKMSPTT+TDPMQKIMTFMPV+FT FFLWFPSGLVLY++VSN+VT+IQQ L

Sbjct: 469 MGASMFVIQKMSPTTITDPMQQKIMTFMPVMFTFFFLWFPSGLVLYWLVSNIPTLIQQL 528

Query: 531 IYRGLEKRGHLSR 543
 IY+ LEK+GLHS+

Sbjct: 529 IYKALEKKGLHSK 541

>ref|YP_128260.1| Putative inner membrane protein, 60 kDa [Photobacterium profundum
 SS9]
 Length = 538

Score = 612 bits (1578), Expect = e-174

Identities = 317/549 (57%), Positives = 398/549 (72%), Gaps = 17/549 (3%)

Query: 1 MDSQRNLLVIALLFVSMIWAWEQDKNPQQAQQTQTQTTTTAAG--SAADQGVPSAGQG 58
 MDSQRN+L+IALLFVSF+++Q W D +PQPQ Q T Q + S + G P Q

Sbjct: 1 MDSQRNILLIALLFVSFLYQQWNMDNSPQPGQGTEQQVNNSGDVPSHSGDGQPIPDQE 60

Query: 59 K----LISVKTDVLDLTINTRGGDVEQALLPAYPKELNSTQPFQLLETSPQFIYQAQSGL 114
 LI++ TDVL L+++T GGDV +A L AY EL+S F LL+ P Y AQSGL

Sbjct: 61 TTSKDLITINTDVLALSVDLTGGDVIEAKLLAYNNELDSDSFILLKDEPGLSYIAQSGL 120

Query: 115 TGRDGPDPNANGPRPLYNVEKDAYVLAEGQNELQVPMTYTDAGNTFTKTFVLKRGDYAV 174
 G +G D+ ANG L KD + LA+GQ+EL+VPMTY G T+TKTFVLKR YAV

Sbjct: 121 IGANGIDS-ANGRAQLAVTAKD-FTLADGQDELRVPMYVVD-GITYTKTFVLKRNSYAV 177

Query: 175 NVNYNVQNAGEKPLEISSFGQLKQSITLPPHLDTGSSNFALHTFRGAAYSTPDEKEYEKYK 234
 +V Y + N + + QL+Q++ +D G S + T+RG AYST Y+KY

Sbjct: 178 DVEYTIDNQSASASVQMYAQLRQNL-----MDDGGS-LTMPTYRGGAYSTDTTNYKKYS 231

Query: 235 FDTIADNENLNISSEKGGWVAMLQQYFATAWIPHNDGTNNFYTANLNGIAAIGYKSQPVL 294

FD + D ++LN+++ GW AMLQ YF +AWIP ++ +N YT NG+ IG +
 Sbjct: 232 FDDMQD-KSLNMTTNGWAAMLQHYFVSAWIPRSEEASNLTY-RASNGLGYIGVRLPTTT 289

Query: 295 VQPGQTGAMNSTLWVGPEIQDKMAAVAPHLDLTVDYGWLWFI SQPLFKLLKWIHSFVGNW 354
 + G + +TLWVGP++Q +M A A +L+LTVDYGWLWFI+ PL KLL +I S VGNW
 Sbjct: 290 IAAGTEQTLTATLWVGPKLQKEMEATAANLNLTVDYGWLWFIASPLHKLLSFIQSIVGNW 349

Query: 355 GFSIIITFIVRGIMYPLTKAQYTSMAKMRMLQPKIQAMRERLGDDKQRISQEMMALYKA 414
 G +I+++TFIVRG MYPLTKAQYTSMAKMRMLQPK+ AMRERLGDD+QR+SQEMM LYK
 Sbjct: 350 GLAIMMLTFIVRGAMYPLTKAQYTSMAKMRMLQPKLTAMRERLGDDRQRMSQEMMELYKK 409

Query: 415 EKNVPLGGCFPLLIQMPIFLALYYMLMGSVELRQAPFALWIHDLAQDPYYILPILMGVT 474
 EKNVPLGGC P+++QMPIF+ALY+ LM SVELR +PF WIHDLAQDPYYILP+LMGV+
 Sbjct: 410 EKNVPLGGCLPIVLQMPIFIALYWSLMESVELRHSPPFGWIHDLAQDPYYILPLLMGVS 469

Query: 475 MFFIQKMSPTTVDTPMQQKIMTFMPVIFTVFFLWFP SGLVLYYIVSNLVTIIQQQLIYRG 534
 MF IQKMSPTTVDTPMQQKIMTFMPV+FT FFL+FPSGLVLY++VSN+VT++QQ LIYR
 Sbjct: 470 MFMIQKMSPTTVDTPMQQKIMTFMPVMFTFFFLFP SGLVLYWLVSNNVTLQQTLIYRS 529

Query: 535 LEKRGHLSR 543
 LEK+GLH++
 Sbjct: 530 LEKKGLHTK 538

>ref|ZP_00201990.1| COG0706: Preprotein translocase subunit YidC [Haemophilus
 influenzae R2846]
 Length = 541

Score = 607 bits (1565), Expect = e-173

Identities = 305/551 (55%), Positives = 397/551 (72%), Gaps = 16/551 (2%)

Query: 1 MDSQRNLLVIALLFVSMIWAWEQDKNPQQAQQTQTTTTA---AGSAADQGV PASGQ 57
 MDS+R+LLV+AL+F+SF+++Q W+ DKNP Q +QTT T T+ A S ++ A Q
 Sbjct: 1 MDSRRSLLVLALIFISFLVYQQWQLDKNPPVQTEQTT SITATSDVPASSPSNSQAIADSQ 60

Query: 58 --GKLISVKTDVLDLTINTRGGDVEQALLPAYPKELNSTQPFQLLETSPQFIYQAQSGLT 115
 G++I+++ DV L I+T GGDV + L Y EL+S PF+LL+ + + IY AQSGL
 Sbjct: 61 TRGRIITLENDVFR LKIDTLGGDVISSELLKYDAELDSKTPFELLKDTKEHIYIAQSGLI 120

Query: 116 GRDGPDPNANGPRPLYNVEKDAYVLAEGQNELQVPMTYTDAGNTFTKTFVLKRGDYAVN 175
 G++G D + R Y +E D + LAEGQ L VP+ + + G T+ K FVLKRG Y +
 Sbjct: 121 GKNGIDTRSG--RAQYQIEGDNFKLAEGQESLSVPLLF-EKDGVTYQKIFVLKRGSYDLG 177

Query: 176 VNYNVQNAGEKPLEISSFGQLKQSITLPPHLD TGSSNFALHTFRGAAYSTPDEKYEKYKF 235
 V+Y + N + +E+ +GQLK SI S N A+ T+ G AYS+ D Y+KY F
 Sbjct: 178 VDYKIDNQSGQAIEVEPYGQLKHSIV-----ESSGNVAMPTYTG GAYSSSDTNYKKYSF 231

Query: 236 DTIADNENLNIS SKGGWVAMLQYFATAWIPHN DGTNNFYT-ANLGNGIAAIGYKSQPVL 294
 + DN NL+I +K GWVA+LQ YF +AWIP+ D N YT + N +A+IGY+ V
 Sbjct: 232 ADMQDN-NLSIDTKAGWVAVLQHYFVSAWIPNQDVNNQLYTITDSKNNVASIGYRGPVVT 290

Query: 295 VQPGQTGAMNSTLWVGPEIQDKMAAVAPHLDLTVDYGWLWFI SQPLFKLLKWIHSFVGNW 354
 + G + +S+LW GP++Q++MA VA +LDLTVDYGW WFI++PLF LL +I V NW
 Sbjct: 291 IPSGSQETITSSLWTGPKLQNMATVANNLDTVDYGWAWFIAKPLFWLLTFIQGIVSNW 350

Query: 355 GFSIIITFIVRGIMYPLTKAQYTSMAKMRMLQPKIQAMRERLGDDKQRISQEMMALYKA 414
 G +II +T +V+ I+YPLTKAQYTSMAKMR+LQPK+Q MRER GDD+QR+SQEMM LYK
 Sbjct: 351 GLAIIICVTIVKAILYPLTKAQYTSMAKMRILQPKMQEMRERFGDDRQRMSQEMMKLYKE 410

Query: 415 EKVNPGLGGCFPLLIQMPIFLALYYMLMGSVELRQAPFALWIHDLAQDPYYILPILMGVT 474
 EKVNPGLGGC P+L+QMPIF+ALY+ + +VELR APF WI DLSAQDPYYILPILMG++
 Sbjct: 411 EKVNPGLGGCLPILLQMPIFIALYWTFLEAVELRHAPFFGWIQDLSAQDPYYILPILMGIS 470

Query: 475 MFFIQKMSPTTVDTPMQQKIMTFMPVIFTVFFLWFPSGLVLYYIVSNLVTIIQQQLIYRG 534
 MF +QKMSPT VTDP QQK+M FMP++F FFLWFPSGLVLY++VSNL+TI QQQLIYRG
 Sbjct: 471 MFLQKMSPTPVDTPMQQKVMNFMPLVFMFFFLWFPSGLVLYWLVSNLITIAQQQLIYRG 530

Query: 535 LEKRGHLSREK 545
 LEK+GLHSR+K
 Sbjct: 531 LEKKGLHSRKK 541

>ref|NP_439163.1| inner membrane protein 60 kDa [Haemophilus influenzae Rd KW20]
 Length = 541

Score = 607 bits (1564), Expect = e-172

Identities = 304/551 (55%), Positives = 397/551 (72%), Gaps = 16/551 (2%)

Query: 1 MDSQRNLLVIALLFVSMIWAWEQDKNPQQAQQTQTTTTA---AGSAADQGVPASGQ 57
 MDS+R+LLV+AL+F+SF+++Q W+ DKNP Q +QTT T T+ A S ++ A Q
 Sbjct: 1 MDSRRSLLVLALIFISFLVYQQWQLDKNPPVQTEQTTTITATSDVPASSPSNSQAIADSQ 60

Query: 58 --GKLISVKTDVLDLTINTRGGDVEQALLPAYPKELNSTQPFQLETSPQFIYQAQSGLT 115
 G++I+++ DV L I+T GGDV + L Y EL+S PF+LL+ + + IY AQSGL
 Sbjct: 61 TRGRIITLENDVFRCLKIDTLGGDVISSELLKYDAELDSKTPFELLKDTKEHIYIAQSGLI 120

Query: 116 GRDGPDPNPANGPRPLYNVEKDAYVLAEGQNELQVPMTYTDAAGNTFTKTFVLKRGDYAVN 175
 G++G D + R Y +E D + LAEGQ L VP+ + + G T+ K FVLKRG Y +
 Sbjct: 121 GKNPIDTRSG--RAQYQIEGDNFKLAEGQESLSVPLLF-EKDGVTYQKIFVLKRGSYDLG 177

Query: 176 VNYNVQNAGEKPLEISSFGQLKQSITLPPHLDTGSSNFALHTFRGAAYSTPDEKYEKYKF 235
 V+Y + N + +E+ +GQLK SI S N A+ T+ G AYS+ + Y+KY F
 Sbjct: 178 VDYKIDNQSGQAIEVEPYQLKHSIV-----ESSGNVAMPTYTGGAYSSSETNYKKYSF 231

Query: 236 DTIADNENLNISSEKGGWVAMLQYFATAWIPHNDGTNNFYT-ANLGNIGIAAIGYKSQPVL 294
 + DN NL+I +K GWVA+LQ YF +AWIP+ D N YT + N +A+IGY+ V
 Sbjct: 232 SDMQDN-NLSIDTKAGWVAVLQHYFVSAWIPNQDVNNQLYTITDSKNNVASIGYRGSVVT 290

Query: 295 VQPGQTGAMNSTLWVGPEIQDKMAAVAPHLDTVDYGWLWFISQPLFKLLKWIHSFVGW 354
 + G + S+LW GP++Q++MA VA +LDLTVDYGW WFI++PLF LL +I V NW
 Sbjct: 291 IPAGSQETITSSLWTGPKLQNMATVANNLDLTVDYGWAWFIAKPLFWLLTFIQGIVSNW 350

Query: 355 GFSIIIIITFIVRGIMYPLTKAQYTSMAKMRMLQPKIQAMRERLGDDKQRISQEMMALYKA 414
 G +II +T +V+ I+YPLTKAQYTSMAKMR+LQPK+Q MRER GDD+QR+SQEMM LYK
 Sbjct: 351 GLAIIICVTIVVKAILYPLTKAQYTSMAKMRILQPKMQEMRERFGDDRQRMSQEMMKLYKE 410

Query: 415 EKVNPGLGGCFPLLIQMPIFLALYYMLMGSVELRQAPFALWIHDLAQDPYYILPILMGVT 474
 EKVNPGLGGC P+L+QMPIF+ALY+ + +VELR APF WI DLSAQDPYYILPILMG++
 Sbjct: 411 EKVNPGLGGCLPILLQMPIFIALYWTFLEAVELRHAPFFGWIQDLSAQDPYYILPILMGIS 470

Query: 475 MFFIQKMSPTTVDTPMQQKIMTFMPVIFTVFFLWFPSGLVLYYIVSNLVTIIQQQLIYRG 534
 MF +QKMSPT VTDP QQK+M FMP++F FFLWFPSGLVLY++VSNL+TI QQQLIYRG
 Sbjct: 471 MFLQKMSPTPVDTPMQQKVMNFMPLVFMFFFLWFPSGLVLYWLVSNLITIAQQQLIYRG 530

Query: 535 LEKRGHLSREK 545
 LEK+GLHSR+K
 Sbjct: 531 LEKKGLHSRKK 541

>ref|ZP_00156859.2| COG0706: Preprotein translocase subunit YidC [Haemophilus
influenzae R2866]
Length = 541

Score = 606 bits (1562), Expect = e-172

Identities = 306/551 (55%), Positives = 397/551 (72%), Gaps = 16/551 (2%)

Query: 1 MDSQRNLLVIALLFVSFMIWQAWEQDKNPQQAQQTQTTTT---AGSAADQGV PASGQ 57
MDS+R+LLV+AL+F+SF+++Q W+ DKNP Q +QTT T T+ A S ++ A Q
Sbjct: 1 MDSRRSLLVLALIFISFLVYQQWQLDKNPPVQTEQTTSITATSDVPASSPSNSQAIADSQ 60

Query: 58 --GKLISVKTDLVLDLTINTRGGDVEQALLPAYPKELNSTQPFQLLETSPQFIYQAQSGLT 115
G++I+++ DV L I+T GGDV + L Y EL+S PF+LL+ + + IY AQSGL
Sbjct: 61 TRGRIITLENDVFRCLKIDTLGGDVISSELLKYDAELDSKTPFELLKDTKEHIYIAQSGLI 120

Query: 116 GRDGPDPNPANGPRPLYNVEKDAYVLAEGQNELQVPMTYTDAAGNTFTKTFVLKRGDYAVN 175
G++G D R Y +E D + LAEGQ L VP+ + + G T+ K FVLKRG Y +
Sbjct: 121 GKNIDTRFG--RAQYQIEGDNFKLAEGQESLSVPLLF-EKDGVTYQKIFVLKRGSYDLG 177

Query: 176 VNYNVQNAGEKPLEISSFGQLKQSITLPPHLDTGSSNFALHTFRGAAYSTPDEKYEKYKF 235
V+Y + N + +E+ +GQLK SI S N A+ T+ G AYS+ + Y+KY F
Sbjct: 178 VDYKIDNQSGQAIEVEPYGQLKHSII-----ESSGNVAMPTYTGGAYSSSETNYKKYSF 231

Query: 236 DTIADNENLNISSKGGWVAMLQOYFATAWIPHNDGTNNFYT-ANLGNGIAAIGYKSQPVL 294
+ DN NL+I +K GWVA+LQ YF +AWIP+ D N YT + N +A+IGY+ V
Sbjct: 232 ADMQDN-NLSIDTKAGWVAVLQHYFVSAWIPNQDVNNQLYTITDSKNNVASIGYRGPVVS 290

Query: 295 VQPGQTGAMNSTLWVGPEIQDKMAAVAPHLDLTVDYGWLWFISQPLFKLLKWIHSFVGNW 354
+ G + S+LW GP++Q++MA VA +LDLTVDYGW WFI++PLF LL +I V NW
Sbjct: 291 IPAGSQETITSSLWTGPKLQNMATVANNLDLTVDYGWAWFIKPLFWLLTFIQGIVSNW 350

Query: 355 GFSIIITFIVRGIMYPLTKAQYTSMAKMRMLQPKIQAMRERLGDDKQRISQEMMALYKA 414
G +II +T +V+ I+YPLTKAQYTSMAKMR+LQPK+Q MRER GDD+QR+SQEMM LYK
Sbjct: 351 GLAIICVTIVVKAILYPLTKAQYTSMAKMRILQPKMQEMRERFGDDRQRMSQEMMKLYKE 410

Query: 415 EKNVPLGGCFPLLIQMPIFLALYYMLMGSVELRQAPFALWIHDLQAQDPYYILPILMGVT 474
EKNVPLGGC P+L+QMPIF+ALY+ + +VELR APF WI DLSAQDPYYILPILMG++
Sbjct: 411 EKNVPLGGCLPILLQMPIFIALYWTFLEAVELRHAPFFGWIQDLQAQDPYYILPILMGIS 470

Query: 475 MFFIQKMSPTTVDTPMQQKIMTFMPVIFTVFFLWFPSGLVLYYIVSNLVTIIQQQLIYRG 534
MF +QKMSPT VTDP QQK+MFMP+IF VFFLWFPSGLVLY++VSNL+TI QQQLIYRG
Sbjct: 471 MFLQKMSPTPVTDPDTPQQKVMNFMPLIFMVFFLWFPSGLVLYWLVSNLITIAQQQLIYRG 530

Query: 535 LEKRGLHSREK 545
LEK+GLHSR+K
Sbjct: 531 LEKKGLHSRKK 541

>ref|NP_246102.1| YidC [Pasteurella multocida subsp. multocida str. Pm70]
Length = 541

Score = 603 bits (1556), Expect = e-172

Identities = 305/551 (55%), Positives = 396/551 (71%), Gaps = 16/551 (2%)

Query: 1 MDSQRNLLVIALLFVSFMIWQAWEQDKN-PQQAQQTQTTT----TAAGSAADQGV PAS 55
MDS+R+LLVIALLF+SF+++Q W+ D + P+P A + + ++ ++A S++D A
Sbjct: 1 MDSRRSLLVIALLFISFLVYQQWQLDYHTPKPVATEQVKVSSDVPASSASSSSDIATTAQ 60

Query: 56 GQGKLISVKTDLVLDLTINTRGGDVEQALLPAYPKELNSTQPFQLETSPOFIYQAQSGLT 115
 QG++I+++ DV L ++T GGDV + L Y ELNS PF LL +Y AQSGL
 Sbjct: 61 AQGRIITLENDVFRLEVDTLGGDVVHSELLKYDAELNSNTPFTLLTNKANHVYIAQSGLV 120

Query: 116 GRDGPDPNPANGPRPLYNVEKDAYVLAEGQNELQVPMTYTDAGNTFTKTFVLKRGDYAVN 175
 G+DG D A R Y V+ D + LA+GQNEL VP + + G TF K FVLKRG Y +
 Sbjct: 121 GKDGDIDTKAG--RANYQVDGDTFKLADGQNELAVPFVF-EKDGVTFRKIFVLKRGAYDIA 177

Query: 176 VNYNVQNAGEKPLEISSFGQLKQSITLPPHLDTGSSNFALHTFRGAAYSTPDEKYEKYKF 235
 VN+ + N +K +E+ +GQL+ ++ DTG N A+ T+ G AYS+ + Y+KY F
 Sbjct: 178 VNFEIDNQSDKTIEVEPYGQLRHTLVE----DTG--NVAMPTYTGGAYSSSETNYKKYSF 231

Query: 236 DTIADNENLNISSKGGWVAMLQQYFATAWIPHNDGTNNFYT-ANLGNIAAIGYKSQPVL 294
 + + NL+IS+K GWVA+LQ YF +AWIP+ D N Y+ + N +A+IGY+
 Sbjct: 232 ADM-EKANLSISTKAGWVAVLQHYFVSAWIPNQDADNQLYSLTDKANNLASIGYRGPVTA 290

Query: 295 VQPGQTGAMNSTLWVGPEIQDKMAAVAPHLDLTVDYGWLWFISQPLFKLLKWIHSFVGNW 354
 + G + S+LW GP++QD+MA VA HLDL+VDYGW WFI++PLF LL +I S V NW
 Sbjct: 291 IPAGAKETIRSSLWTGPKLQDQMATVANHLDSLVDYGWAWFIKPLFWLLTFIQSIVQNW 350

Query: 355 GFSIIITFIVRGIMYPLTKAQYTSMAKMRMLQPKIQAMRERLGDDKQRISQEMMALYKA 414
 G +II +T +V+ I+YPLTKAQYTSMAKMRMLQPK+Q MRER G+D+QR+SQEMM LYK
 Sbjct: 351 GLAIIGVTLVKAILYPLTKAQYTSMAKMRMLQPKLQEMRERFGEDRQRMSQEMMKLYKE 410

Query: 415 EKVNPGLGGCFPLLIQMPIFLALYYMLMGSVELRQAPFALWIHDLAQDPYYILPILMGVT 474
 EKVNPGLGGC P+L+QMPIF+ALY+ + +VELR APF WI DLSAQDPYYILPILMG +
 Sbjct: 411 EKVNPGLGGCLPILLQMPIFIALYWTFLEAVELRHAPFFGWIQDLSAQDPYYILPILMGAS 470

Query: 475 MFFIQKMSPTTVTDPMQQKIMTFMPVIFTVFFLWFPSGLVLYYIVSNLVTIIQQQLIYRG 534
 MF +QKMSPT V DP QQKIM FMP+IF VFFLWFPSGLVLY++VSNL+TI QQQLIYRG
 Sbjct: 471 MFLQKMSPTPVADPTQQKIMNFMPLIFMVFFLWFPSGLVLYWLVSNLITIAQQQLIYRG 530

Query: 535 LEKRGLHSREK 545
 LEK+GLHSR K
 Sbjct: 531 LEKKGLHSRHK 541

>ref|ZP_00134946.2| COG0706: Preprotein translocase subunit YidC [Actinobacillus
 pleuropneumoniae serovar 1 str. 4074]
 Length = 542

Score = 602 bits (1551), Expect = e-171
 Identities = 305/554 (55%), Positives = 394/554 (71%), Gaps = 21/554 (3%)

Query: 1 MDSQRNLLVIALLFVSFMIWQAWEQDKNPQQAQQTQTTTTAAGSAADQGVPSG---- 56
 M+S R+LLV+ LL VSF+I+ W+QD NP+ QQA+ Q A + D ++
 Sbjct: 1 MNSNRSLLVMLGLLVSFLLIFTQWQQDFNPEIQAKQAQQQAQVASQSGDVLAASNANTVI 60

Query: 57 -----QGKLISVKTDLVLDLTINTRGGDVEQALLPAYPKELNSTQPFQLETSPOFIYQAQ 111
 QGK +++++DVL LTI+T GGDV + L A+ ELNS PF+LL+T Y AQ
 Sbjct: 61 AENATQGKTVTLES DVLRLTIDTLGGDVIA SDLLAHNAELNSQT PFKLLQTGAT-TYVAQ 119

Query: 112 SGLTGRDGPDPNPANGPRPLYNVEKDAYVLAEGQNELQVPMTYTDAGNTFTKTFVLKRGD 171
 SGL G++G D N RP Y V +D +VLAEGQNE+ VPMT+ + G +TKTFVLKRG
 Sbjct: 120 SGLVGKNGIDT--NAGRPQYQVAQDTFVLAEGQNEMSVPMTF-EKDGVLTKTFVLKRG 176

Query: 172 YAVNVNQNAGEKPLEISSFGQLKQSITLPPHLDTGSSNFALHTFRGAAYSTPDEKYE 231
 Y V VN+NV+N +E+ +GQ+K ++ S + + T+ G AYS+ + Y+

Sbjct: 177 YDVAVNFNVKNQTAATVEVQPYGQIKHTLL-----ESSGSLTMPYTGAYSSAETNYK 230

Query: 232 KYKFDTIADNENLNISSEKGGWVAMLQQYFATAWIPHNDGTNNFYTANLGNIAAIGYKSQ 291
KY F + + NL+I++K GWVA+LQ YF +AW+P+ D N Y+ NGIA IGY+

Sbjct: 231 KYSFQDM-EKANLDINTKAGWVALLQHYFVSAWVPNQDAENTIYSRT-NNGIATIGYRGP 288

Query: 292 PVLVQPGQTGAMNSTLWVGPEIQDKMAAVAPHLDLTVDYGWLWFISQPLFKLLKWIHSFV 351
+ P + S LW GP+ Q +M A A +LDLTVDYGW WFI++PLF LL +I S V

Sbjct: 289 VTTIAPNSEATITSQLWTGPKDQKEMEATAANLTLVDYGWAWFIAKPLFALLTFIQSIV 348

Query: 352 GNWGFSSIIITFIVRGIMYPLTKAQYTSMAKMRMLQPKIQAMRERLGDDKQRISQEMMAL 411
NWG +II +T +V+ I+YPLTKAQYTSMA+MRMLQPKIQ MRER GDD+QR+SQEMM L

Sbjct: 349 TNWGLAIIGVTIVVKTILYPLTKAQYTSMAKMRMLQPKIQEMRERFGDDRQMSQEMMKL 408

Query: 412 YKAEKVNPLGGCFPLLIQMPIFLALYYMLMGSVELRQAPFALWIHDLAQDPYYILPILM 471
YK EKNP+GGC P+LIQMPIF+ALY+ M +VELR APF WI DLSAQDPYYILP+LM

Sbjct: 409 YKEEKVNPMGGCLPILIQMPIFIALYWFMEAVELRHAPFFGWIQDLAQDPYYILPLLM 468

Query: 472 GVTMFFIQKMSPTTVDTPMQQKIMTFMPVIFTVFLLWFPSGLVLYIVSNLVTIIQQQLI 531
G +MF +QKMSP+ VTDP+QK+MTFMPV+FTVFLLWFPSGLVLY++ SN++TI+QQ LI

Sbjct: 469 GASMFLLQKMSPSPVTDVPVQKVMFTFMPVMTVFLLWFPSGLVLYWLTSNIITIVQQWLI 528

Query: 532 YRGLEKRGHLSREK 545
YR LEK+GLHSR+K

Sbjct: 529 YRNLEKKGLHSRKK 542

>ref|NP_777655.1| putative membrane protein [Buchnera aphidicola str. Bp (Baizongia pistaciae)]
Length = 536

Score = 597 bits (1538), Expect = e-169

Identities = 287/541 (53%), Positives = 393/541 (72%), Gaps = 12/541 (2%)

Query: 1 MDSQRNLLVIALLFVSMIWAWEQDKNPQQAQQTQTOTTTTAAGSAADQGV PASGQK 60
M QRN ++ F+SF++W+ W+Q ++ + + + KL

Sbjct: 1 MHLQRNFFILIFFFISFLLWKTWQQ-----KEFSSDVHKKIINKYENVNLVNNINKL 52

Query: 61 IS---VKTDVLDLTINTRGGDVEQALLPAYPKELNSTQPFQLETSQFIYQAQSGLTGR 117
S +KTDVL + +N GGD+E+A L + +LNS+Q LL+T+ F+YQAQ G+TG+

Sbjct: 53 ASNIIIKTDVLKIQVNLYGGDIEKAELLHFKSKLNSQSLVLLDTNENFVYQAQCGITGK 112

Query: 118 DGPDPNANGPRPLYNVEKDAYVLAEGQNELQVPMTYTDAGNTFTKTFVLKRGDYAVNVN 177
DG DN RPLY ++ Y L+ +++VP+ + G + K FVLK G+Y V+V

Sbjct: 113 DGADNLQKHIRPLYIAKRKYELSRHNKKIEVPLQWISKDGIYKKIFVLKSGEYDVSVK 172

Query: 178 YNVQNAGEKPLEISSFGQLKQSITLPPHLDTGSSNFALHTFRGAAYSTPDEKYEKYKFDT 237
Y + N K L++S FGQLKQ+I LP +T ++NFAL TFRGAAYS+ ++KY KY FD+

Sbjct: 173 YKINNITNKHLLKVSFMFGQLKQTINLPEDKNTYTNNFALQTFRGAAYSSDNDKYVKYSFDS 232

Query: 238 IADNENLNIS-SKGGWVAMLQQYFATAWIPHNDGTNNFYTANLGNIAAIGYKSQPVLVQ 296
I + E NI + GWVAMLQ+YFAT+WIP N N Y + G+ +A IGY S+P+ +

Sbjct: 233 IVNKEKKNIVVTHSGWVAMLQKYFATSWIPDNSYLNMTYIGSSGDNLAIGYYSRPIDIF 292

Query: 297 PGQTGAMNSTLWVGPEIQDKMAAVAPHLDLTVDYGWLWFISQPLFKLLKWIHSFVGNWGF 356
P T +++S LW+GPEIQ+KMA +A +LDLTVDYGWLWF+SQPLFKLL +++ GNWG

Sbjct: 293 PHSTISLSSKLWIGPEIQNKMAVIASNLDLTVDYGWLWFLSQPLFKLLNFLYNICGNWGV 352

Query: 357 SIIITFIVRGIMYPLTKAQYTSMAKMRMLQPKIQAMRERLGDDKQRISQEMMALYKAEK 416

SII+ITFI++GI +PLTK+Q+ +MAK+R LQPKI +++++ ++ Q+IS+E+M+LYK EK
 Sbjct: 353 SIILITFIIKGITFPLTKSQFKTMAKIRKLQPKINYIKKKFKNNNQKISEEIMSLYKTEK 412

Query: 417 VNPLGGCFPLLIQMPIFLALYYMLMGSVELRQAPFALWIHDLQAQDPYYILPILMGVTMF 476
 VNPLGGCFPL IQMPIFLALYYML+ SVELR APF LWIHDLS QDP+Y+LPILMGVTMF
 Sbjct: 413 VNPLGGCFPLFIQMPIFLALYYMLISSVELRHAPFFLWIHDLSDQDPFYVLPILMGVTMF 472

Query: 477 FIQKMSPTTVDPMQKIMTFMPVIFTVFLLWFPSGLVLYYIVSNLVTIIQQQLIYRGL 536
 FIQ+++P+ VTDP+Q+KIM ++P++FTVFLLWFPSGLVLYY++SNLVTIIQQ++I + L
 Sbjct: 473 FIQRTVPSNVTDPVQKIMNYIPILFTVFLLWFPSGLVLYYLISNLVTIIQQKIIKALN 532

Query: 537 K 537
 K
 Sbjct: 533 K 533

>ref|ZP_00133087.2| COG0706: Preprotein translocase subunit YidC [Haemophilus somnus
 2336]
 Length = 541

Score = 592 bits (1525), Expect = e-168
 Identities = 295/551 (53%), Positives = 397/551 (72%), Gaps = 15/551 (2%).

Query: 1 MDSQRNLLVIALLFVSFMIWQAWEQDKN-PQPQAQ---QTTQTTTTAAGSAADQGVPSAG 56
 MDS+R+LL +ALLF+SF+I+Q W+ D N P+P+ Q ++ +TA + +D
 Sbjct: 1 MDSKRSLLFMALLFISFLIYQQWQVDYNTPKPEVTEQAQVSEVNSTALTATSDIANDTQA 60

Query: 57 QGKLISVKTDVLDLTINTRGGDVEQALLPAYPKELNSTQPFQLETSPQFIYQAQSGLTG 116
 +G++I+++ DV L +NT GGDV + L Y EL+S+ PF LL+ + +Y AQSG L G
 Sbjct: 61 KGRVITLENDVFRLLKVNTLGGDVIGSELLNYDAELHSSAPFVLLQNNADKVYIAQSGLVG 120

Query: 117 RDGPDNPANGPRPLYNVEKDAYVLAEGQNELQVPMTYTDAAGNTFTKTFVLKRGDYAVNV 176
 ++G D+ A R Y VE D + LAEGQ EL+VP+ + + G + K FVLK G YA+ V
 Sbjct: 121 KNGIDSRA--RANYQVEGDVFKLAEGQQLKVPLIF-EKDGVIYRKVFVLKPGSYALEV 177

Query: 177 NYNVQNAGEKPLEISSFGQLKQSITLPPHLDTGSSNFALHTFRGAAYSTPDEKEYEKYKFD 236
 N+ + N KP+E+ + QL ++ S + A+ T+ G AYS+ + Y+KY F+
 Sbjct: 178 NFEITNQSPKPIELVPYAQLTHTLV-----ESSGSMAMPTYTGGAYSSSETNYKKYSFE 231

Query: 237 TIADNENLNISCKGGWVAMLQQYFATAWIPHNDGTNNFYT-ANLGNIAAIGYKSQPVLV 295
 + + +L+I +K GWVA+LQ YF +AWIP+ D N YT N + +IGY+S P+++
 Sbjct: 232 DM-EKADLDIHTKAGWVALLQHYFVSAWIPNQDANNTLYTLTNTKKHLGSIGYRSAPIVI 290

Query: 296 QPGQTGAMNSTLWVGPEIQDKMAAVAPHLDTVDYGLWLFISQPLFKLLKWIHSFVGNWG 355
 + G T +++ LW GP++QD+MA VA HLDLTVDYGW WFI++PLFKLL I S V NWG
 Sbjct: 291 ENGATETIHTQLWTGPKLQDQMDADVANHLDLTVDYGWAWFIAKPLFKLLTLIQSLVQNWG 350

Query: 356 FSIIITFIVRGIMYPLTKAQYTSMAKMRMLQPKIQAMRERLGDDKQRISQEMMALYKAE 415
 +II +T +V+ ++YPLTKAQYTSMAKMRMLQPK+Q MRER G+D+QR+SQEMM LYK E
 Sbjct: 351 LAIIGVTLVVKAVLYPLTKAQYTSMAKMRMLQPKLQEMRERFGEDRQRMSQEMMKLYKEE 410

Query: 416 KVNPLGGCFPLLIQMPIFLALYYMLMGSVELRQAPFALWIHDLQAQDPYYILPILMGVTM 475
 KVNPLGGC P+L+QMPIF+ALY+ M +VELR APF W+ DLSAQDPY+ILPILMG +M
 Sbjct: 411 KVNPLGGCLPILLQMPIFIALYWTFMEEAELRHAPFFGWVQDLSAQDPYFILPILMGASM 470

Query: 476 FFIQKMSPTTVDPMQKIMTFMPVIFTVFLLWFPSGLVLYYIVSNLVTIIQQQLIYRGL 535
 F +QKMSPT V DPMQK+MTFMP+IF VFLL+FP+GLVLY++ SNL+TI QQ LIYRGL
 Sbjct: 471 FLLQKMSPTPVADPMQKQVMTFMPLIFMVFFLFFPAGLVLYWLASNLITIAQQWLIYRGL 530

Query: 536 EKRGLHSREKK 546
 EK+GLH+R KK
 Sbjct: 531 EKKGLHTRVKK 541

>ref|NP_872666.1| 60 kD inner-membrane protein [Haemophilus ducreyi 35000HP]
 Length = 536

Score = 589 bits (1519), Expect = e-167
 Identities = 299/548 (54%), Positives = 394/548 (71%), Gaps = 15/548 (2%)

Query: 1 MDSQRNLLVIALLFVSFMIWQAWEQDKNPQPQAQQTQTTTT---AGSAADQGV PASGQ 57
 M+S R+LLV+ LL VSF+I+ W+QD NP+ QAQ+ Q + A + A+ +
 Sbjct: 1 MNSNRSLVMGLLLVSFLIFTQWQQDFNPEIQAKQAQQQSRDVP HATNTANAITEHMTK 60

Query: 58 GKLISVKTDVLDLTINTRGGDVEQALLPAYPKELNSTQPFQLETSPQFIYQAQSGLTGR 117
 GK I+V++DVL L I+T GGDV ++ L A+ L+ST P +LL T+ IY AQSG L G+
 Sbjct: 61 GKTITVESDVLRLVIDTLGGDVIESDLLAHKASLDSTDPLKLL-TTEGLIYTAQSGLVGK 119

Query: 118 DGPDNPANGPRPLYNVEKDAYVLAEGQNELQVPMTYTDAAGNTFTKTFVLKRGDYAVNVN 177
 +G D R Y V +D + LA+GQNE+ VPMT+ + G +TKTF LKRG Y V V+
 Sbjct: 120 NGIDTHIG--RAPYQVTQDHFTLAKGQNEIVVPMTF-EQDGVMYTKTFTLKRGSYDVAVS 176

Query: 178 YNVQNAGEKPLEISSFGQLKQSITLPPHLDTGSSNFALHTFRGAAYSTPDEKYEKYKFD 237
 +++QN +E+ +GQ+K S+ LD+ S N A+ T+ G AYS+ + Y+KY FD
 Sbjct: 177 FDIQNN SANTIEVQPYGQIKHSL-----LDS-SGNLAMPYTG GAYSSSETNYKKYSFDE 230

Query: 238 IADNENLNIS SKGGWVAMLQQYFATAWIPHNDGTNNFYTANLNGIAAIGYKSQPVLVQP 297
 + NLNI +KGGWVA+LQ YF +AW+P+ D +N Y+ NG+A IGY+ V+P
 Sbjct: 231 MT-KANLNIDTKGGWVALLQHYFVSAWVPNQDASNTLYSRT-HNGVATIGYRGPIITTVKP 288

Query: 298 GQTGAMNSTLWVGPEIQDKMAAVAPHLDLTVDYGWLWFISQPLFKLLKWIHSFVGNWGFS 357
 + S LW GP+ Q +MA A HL+LTVDYGW WFI++PLF LL +IHS +GNWG +
 Sbjct: 289 NTKTTITSQLWTGPKDQKEMAQAATHLELTVDYGWAWFIAKPLFWLLIFIHSIIGNWGLA 348

Query: 358 IIIITFIVRGIMYPLTKAQYTSMAKMRMLQPKIQAMRERLGDDKQRISQEMMALYKAKEV 417
 I+ +T +V+ ++YPLTKAQYTSMAKMRMLQPK+Q +RER GDD+Q++SQEMM LYK EKV
 Sbjct: 349 IMGVTLVVKSLLYPLTKAQYTSMAKMRMLQPKLQELRERYGDDRQMSQEMMKLYKQEKV 408

Query: 418 NPLGGCFPLLIQMPIFLALYYMLMGSVELRQAPFALWIHDL SAQDPYYILPILMGVTMFF 477
 NP+GGC PL++QMPIF+ALY+ M +VELR APF WI DLSAQDPYYI P+LMG++MF
 Sbjct: 409 NPMGGCLPLILQMPIFIALYWTFMEAVELRHAPFFGWIQDLSAQDPYYIFPVLMLGSLMFL 468

Query: 478 IQKMSPTTVDTPMQQKIMTFMPVIFTVFFLWFPSGLVLVYIVSNLVTIIQQQLIYRGLEK 537
 +QKMSPT V DP Q K+MTFMPVIFTVFFLWFPSGLVLVY++ SN +TI+QQ LIYR LEK
 Sbjct: 469 LQKMSPTAVADPTQLKVMTFMPVIFTVFFLWFPSGLVLVWLT SNCITIVQQWLIYRNLEK 528

Query: 538 RGLHSREK 545
 +GLH+R+K
 Sbjct: 529 KGLHTRKK 536

>ref|NP_715646.1| inner membrane protein, 60 kDa [Shewanella oneidensis MR-1]
 Length = 541

Score = 570 bits (1469), Expect = e-161
 Identities = 288/549 (52%), Positives = 385/549 (70%), Gaps = 16/549 (2%)

Query: 1 MDSQRNLLVIALLFVSFMIWQAWEQDKNPQQAQQT-----QTTTAAAGSAADQGV PAS 55
M+SQRN+L+I LLEVFSF++WQ W+ DK P+P A +++ T +A AD GVPA+
Sbjct: 1 MESQRNILLIGLLFVSFLLWQQWQADKAPKPVATESSVVANATTNHSADVPEADTGVPA 60

Query: 56 --GQGKLISVKTDVLDLTINTRGGDVEQALLPAYPKELNSTQPFQLETSPOFIYQAQSG 113
LI+VKTD LD+ IN GGD+ A L ++ E QPF LLE + F Y AQSG
Sbjct: 61 VAATQNLITVKTDQLDVQINPVGDIVYAALVSHKLEQKQDPFVLLEQTKDFTYIAQSG 120

Query: 114 LTGRDGPDPNPANGPRPLYNVEKDAYVLAEGQNELQVPMYTDAGNTFTKTFVLKRGDYA 173
L GRDG D+ A G R ++ K + LA+GQ+ L+VP+TY G T+TK FV RG +
Sbjct: 121 LIGRDGIDSSAKG-RAIFAASKTEFTLADGQDSLEVPLTYVAENGVTYTKVVFVHRGKFN 179

Query: 174 VNVNYNVQNAGEKPLEISSFGQLKQSITLPPHLDTGSSNFALHTFRGAAYSTPDEKYEKY 233
VN++Y + N PL++ +GQ+KQ+I S+ + T+RGAA+ST +YEKY
Sbjct: 180 VNIDYKINNTSAAPLQVQMYGQIKQTIK-----PSESSMMPTYRGAAFSTASVRYEKY 233

Query: 234 KFDTIADNENLNISKGGWVAMLQOYFATAWIPHNDGTNNFYTANLGNIAAIGYKSQPV 293
F+ + N NLN + GGW AMLQ YF +AWIP +N +++ G+A IG++
Sbjct: 234 NFEDMGKN-NLNQPTIGGWAAMLQHYFVSAWIPPATDSNTIFSSVSAGGLANIGFRGAVY 292

Query: 294 LVQPGQTGAMNSTLWVGPEIQDKMAAVAPHLDTVDYGWLWFISQPLFKLLKWIHSFVGN 353
V PG T ++S +VGP+ Q ++A++ L+L VDYG+LW+++ P+ LL + SFVGN
Sbjct: 293 DVAPGATQEISSQFYVGPDKQKALSALSDTLNLVVDYGFLWWLAVPIHWLLMFYQSFVGN 352

Query: 354 WGFSIIITFIVRGIMYPLTKAQYTSMAKMRMLQPKIQAMRERLGGDKQRISQEMMALYK 413
WG +II+IT VRG+++PLTKAQYTSMAKMR LQPK+Q ++ER GDD+Q++ Q MM LYK
Sbjct: 353 WGVAILITLTVRGLLFPLTKAQYTSMAKMRNLQPKLQDLKERFGDDRQKMGQAMMELYK 412

Query: 414 AEKVNPLGGCFPLLIQMPIFLALYMLMGSVELRQAPFALWIHDLQAQDPYYILPILMGV 473
EKNVP+GGC P+L+QMPIF+ALY++L+ S ELR APF LWIHDLS QDPYYILP+LMGV
Sbjct: 413 KEKVNPMGGCLPILLQMPIFIALYVWLLESFELRHAPFMLWIHDLVQDPYYILPILMGV 472

Query: 474 TMFFIQKMSPTTVT-DPMQKIMTFMPVIFTVFFLWFPSGLVLYYIVSNLVTIIQQQLIY 532
+MF +QKM P T DPMQ K+M +MPVIFTVFFLWFPSGLVLY++V N+V IIQQ++IY
Sbjct: 473 SMFIMQKMQPIAPTMDPMQVMMQWMPVIFTVFFLWFPSGLVLYVWLVGNIVAIQQKIY 532

Query: 533 RGLEKRGHLH 541
GLEK+GL+
Sbjct: 533 AGLEKKGLN 541

>ref|NP_871016.1| yidC [Wigglesworthia glossinidia endosymbiont of Glossina
brevipalpis]
Length = 540

Score = 538 bits (1386), Expect = e-152

Identities = 268/538 (49%), Positives = 374/538 (69%), Gaps = 4/538 (0%)

Query: 4 QRNLLVIALLFVSFMIWQAWEQDKNPQQAQQTQTTTAAAGSAADQGV PASGQGKLISV 63
Q N L IA +FV+FM+ AW Q ++ ++ + + I+V
Sbjct: 4 QNNFLFIAFIFVTFMMLDAW-QSESYDYKSLDKNHIIEKKNINENKEVFSRENYITV 62

Query: 64 KTDVLDLTINTRGGDVEQALLPAYPKELNSTQPFQLETSPOFIYQAQSGLTGRDGPDPNP 123
TD+ L INT GGD+E+A L Y + P ++L+ S FIY+ +SG ++ D
Sbjct: 63 ITDLFILKINTYGGDIEEASLRYSNTKNNLPLKILDRSKNFIYKLKSGFITKNDHDIN 122

Query: 124 ANGPRPLYNVEKDAYVLAEGQNELQVPMYTDAGNTFTKTFVLKRGDYAVNVNYNVQNA 183
P + +K Y+L + + LQVP+ Y G + K F+ K+ +++ +NY+++N
Sbjct: 123 NLIHIPNFISDKKLYILEDNSDYLVPLFYNGENGLKYVKNFIFKKNSFSLKINYSIKNT 182

Query: 184 GEKPLEISSFGQLKQSITLPPHLDTGSSNFALHTFRGAAYSTPDEKYEKYKFDTIADNEN 243
 + +E+ FGQL+QSI ++ G NF HT+RGAAYS+ + KY+KY F I++++N
 Sbjct: 183 NKDKMEMMFFGQLEQSIK-DQEINNGY-NFNFTYRGAAYSSDNNKYKYDFSEISNDKN 240

Query: 244 LNISSKGGWVAMLQQYFATAWIPHNDGTNNFYTANLGNGI-AAIGYKSPVLVQPGQTGA 302
 LN+ + GW+AMLQQYF AWIP + FYT N+ +IG++S+ + +
 Sbjct: 241 LNVITSNGWIAMLQQYFIVAWIPKIENKYKFYTKNIPKDEKVSIGFQSELFSDQEEKN 300

Query: 303 MNSTLWVGPEIQDKMAAVAPHLDTVDYGWLWFISQPLFKLLKWIHSFVGNWGFSSIIIT 362
 + STLW+GP++QDKM V +L LTVDYGWLWFI+QPL +LLK+I+ ++ NWG SIIIT
 Sbjct: 301 IESTLWIGPKLQDKMYEVDANLGLTVDYGWLWFIAQPLLQLLKFIYKYINNNGISIIIT 360

Query: 363 FIVRGIMYPLTKAQYTSMAKMRMLQPKIQAMRERLGDDKQRISQEMMALYKAQKVNPLGG 422
 F+VRGIM+PLTKAQYTSMAKMR+LQPKI ++ + +DK+R S+EMM+LYK +KVNPLGG
 Sbjct: 361 FMVRGIMFPLTKAQYTSMAKMRILQPKIIEIKNKFSDKKRQSKEMMSLYKKQKVNPLGG 420

Query: 423 CFPLLIQMPIFLALYYMLGSVELRQAPFALWIHDLAQDPYYILPILMGVTMFFIQKMS 482
 C PL+IQMPIFLALYYML GSVELR A F LWI+DLS++DPYYILPI+MG+TMF IQK+S
 Sbjct: 421 CMPLIIQMPIFLALYYMLSGSVELRHAHFVLWINDLSSKDPYYILPIIMGITMFLIQKIS 480

Query: 483 PTTVTDPMQKIMTFMPVIFTVFFLWFPSGLVLYYIVSNLVTIIQQQLIYRGLEKRG 540
 P++++DP+Q+KI++FMP+IFT+FFLWFPSGLVLYYI+SNLVTIIQQ +IY+ L+K G+
 Sbjct: 481 PSSISDPVQKIVSFMPILIFTIFFLWFPSGLVLYYIISNLVTIIQQYIIYKDLKKVGI 538

>ref|NP_878327.1| putative Preprotein translocase subunit YidC [Candidatus
 Blochmannia floridanus]
 Length = 558

Score = 528 bits (1360), Expect = e-149
 Identities = 275/559 (49%), Positives = 367/559 (65%), Gaps = 16/559 (2%)

Query: 1 MDSQRNLLVIALLFVSFMIWQAWEQDKNPQQAQOTTQTTT---TAAGSAADQGV PASGQ 57
 M+SQR+ +I L VSF++W+ W+ + + + +T + ++Q P +
 Sbjct: 1 MESQRSFFIIVFLIVSFILWKIWDDEHHINLLNIENNHS TLQPYSIQSHESNQNTPIHT 60

Query: 58 GK----LISVKTDLVLDLTINTRGGDVEQALLPAYPKELNSTQPFQLETSPQFIYQAQSG 113
 +I++KTDV L INT G++E+A L Y + LNS +P +LL TS + YQA
 Sbjct: 61 NNPYSHIITIKTDVFLKINTYSGNIEEAYLNNYQENLNSQKPLKLLHTSKENKYQAYID 120

Query: 114 LTGRD----GPDNPANGPRPLY---NVEKDAYVLAEGQNELQVPMTYTDAAGNTFTKTFV 166
 + + N N LY + Y+L +N+LQ +TY +TK ++
 Sbjct: 121 IETLNEYFTNDLNQKNKKHYLYSNTTNQCEYILKNNENKLQFDLTYQGPNNIYTKRYL 180

Query: 167 LKRGDYAVNVNYNVQNAGEKPLEISSFGQLKQSITLPPHLDTGSSNFALHTFRGAAYSTP 226
 L R DY++ + Y + N P+ I +G L QSI + + L+T++ AAYST
 Sbjct: 181 LNRNDYSIYITYIIDNQSTYPIHIKLYGNLIQSIHSDVIQSKHNDHCPLYTYQEAAYSTD 240

Query: 227 DEKYEKYKFDTIADNENLNISSKGGWVAMLQQYFATAWIPHNDGTNNFYTANLGNGIAAI 286
 EKY+KY I + NLNI S GW+A+LQ+YF A +P N FYT L N +I
 Sbjct: 241 TEKYQKYNLKD IK-HTNLNIHSTNGWIAL LQKYFIIALLPITPKDNTFYTTYLNNHDISI 299

Query: 287 GYKSPVLVQPGQTGAMNSTLWVGPEIQDKMAAVAPHLDTVDYGWLWFISQPLFKLLKW 346
 G+KS + + PG+ + S LW+GP+IQD M VAP+LDL +DYGWLWFIS PLFKLL++
 Sbjct: 300 GFKSDFIHIPP GKKNELQSILWMGPKIQDNMKLVAPNLDLVIDYGWLWFISHPLFKLLQF 359

Query: 347 IHSF-VGNWGFSSIIITFIVRGIMYPLTKAQYTSMAKMRMLQPKIQAMRERLGDDKQRIS 405
 IH++ + NWG SII+IT I+R IMYPLTKAQYTSMAK+RMLQPK+ +++E DK +

Sbjct: 360 IHTYTIDNWGISIILITVIIRLIMYPLTKAQYTSMAKIRMLQPKLISIQEEYKHKDYQYH 419

Query: 406 QEMMALYKAEKVNPLGGCFPLLIQMPIFLALYYMLMGSVELRQAPFALWIHDLQAQDPYY 465
Q+ + LYK EKNPLGGC PLLIQMPIFLALYYML SVELR A FA WI DLS QDPYY

Sbjct: 420 QKTIELYKKEKVNPLGGCLPLLIQMPIFLALYYMLSESVELRHAKFAFWIKDLSQDPYY 479

Query: 466 ILPIIMGVMTFFIQKMSPTTVDTPMQQKIMTFMPVIFTVFFLWFPISGLVLYYIVSNLVTI 525
ILPI+MG+TMFFIQK+SPTT+TDP+Q+KIM M VIFT+FFLWFPISGLVLYYI+SN++TI

Sbjct: 480 ILPIIMGITMFFIQKLSPTTITDPIQKKIMNIMLVIFTIFFLWFPISGLVLYYIISNIITI 539

Query: 526 IQQQLIYRGLEKRGHLSRE 544
IQQQ+IY L K+GLH+++

Sbjct: 540 IQQQVIYHDLSSKGLHNKK 558

>ref|ZP_00091071.1| COG0706: Preprotein translocase subunit YidC [Azotobacter
vinelandii]
Length = 557

Score = 478 bits (1229), Expect = e-134
Identities = 249/559 (44%), Positives = 360/559 (64%), Gaps = 29/559 (5%)

Query: 1 MDSQRNLLVIALLFVSFMIWQAWEQD-----KNPQPQAQQTQTQTTTAAGSAADQGV 52
MD +R++L++AL VS+++ W QD +N Q+ T S+ V

Sbjct: 1 MDIKRSILLVALAVSYLLVLQWNQDYGQAALPPQNAVAQSASPALPETVPGDSSTSADV 60

Query: 53 PASGQGK-----LISVKTDVLDLTINTRGGDVEQALLPAYPKELNSTQ-PFQ 98
P +G G LI V+TDVL++ I+ RGGD+ Q LP +P+ + + PFQ

Sbjct: 61 PTAGSGNQVPDSAASTAGSDLIQVRTDVLEVAIDPRGGDIVQLKLPKFPRRQDHPEIPFQ 120

Query: 99 LLETSPQFIYQAQSGLTGRDGPDPNPANGPRPLYNVEKDAYVLAEGQNELQVPMYTYTDAAG 158
L + + +Y AQSGLTG +GPD A+G RPLY E+ +Y LA+GQ+ L V + ++D G

Sbjct: 121 LFDNGSERLYLAQSGLTGTNGPDARADG-RPLYVSEQRSYQLADGQDSLVDLKFSDG-G 178

Query: 159 NTFTKTFVLKRGDYAVNVNYNVQNAGEKPLEISSFGQLKQSITLPPHLDTGSSNFALHTF 218
+ K F KRG Y + V + + N E+P + F QLK+ + P T + T+

Sbjct: 179 VDYVKRFTFKRGAYDLEVRHQIANHSEQPWSGNLFAQLKRDASADPSSTTATGTA---TY 235

Query: 219 RGAAYSTPDEKEYEKYKFDTIADNENLNISSEKGGWVAMLQQYFATAWIPHNDGTNNFYTAN 278
GAA T +E Y K + D++NL + +GGWVA LQ YF TAW+P+ D TN T

Sbjct: 236 LGAALWTSEEPYRKVSMGDM-DDKNLRETQGGWVAWLQHYFVTAWVPNKDDTNLVATRK 294

Query: 279 LGNGIAAIGYKSPVLVQPGQTGAMNSTLWVGPEIQDKMAAVAPHLDLTVDYGWLWFISQ 338
G IG+ + + G TG + L+ GP+ Q+++ A++P L+LTVDYG+LWFI+Q

Sbjct: 295 DSQGNYYIGFTGSTLNIPAGATGETVTRLYAGPKDQNLQLEALSPGLELTVDYGFLWFIAQ 354

Query: 339 PLFKLLKWIHSFVGNWGFSSIIITFIVRGIMYPLTKAQYTSMAKMRMLQPKIQAMRERLG 398
P+F LL+ IH+ +GNWG+SII++T I++ +PL+ A Y SM +MR + PK+QA++E+ G

Sbjct: 355 PIFWLLELIHALLGNWGSIIIVLTVIIKLAFFPLSAASYRSMGRMRAPKLQALKEQHG 414

Query: 399 DDKQRISQEMMALYKAEKVNPLGGCFPLLIQMPIFLALYYMLMGSVELRQAPFALWIHDL 458
+D+Q++SQ MM LYK EK+NPLGGC P+L+QMP+FLALY++L+ SVE+RQAP+ WI DL

Sbjct: 415 EDRQKLSQAMMELYKKEKINPLGGCLPILVQMPVFLALYWVLLESVEMRQAPWLGWITDL 474

Query: 459 SAQDPYYILPIIMGVMTFFIQKMSPTTVDTPMQQKIMTFMPVIFTVFFLWFPISGLVLYYI 518
S +DPY+ILPI+MG TMFF Q ++PT DPMQ ++M MP+IFT FFLWFP+GLVLY++

Sbjct: 475 SVKDPYFILPIIMGATMFFQQTNLNTP-PDPMQARVMKLMPIIFTFFFLWFPAGLVLYWV 533

Query: 519 VSNLVTIIQQQLIYRGLEK 537

V+N+++I QQ I R +EK

Sbjct: 534 VNNVLSIGQQWYITRQIEK 552

>ref|NP_742176.1| inner membrane protein, 60 kDa [Pseudomonas putida KT2440]
Length = 560

Score = 475 bits (1223), Expect = e-133

Identities = 255/561 (45%), Positives = 348/561 (62%), Gaps = 34/561 (6%)

Query: 1 MDSQRNLLVIALLFVSFMIWQAWEQDKNPQQAQQTQTTTTAAGSAADQGVPA SGQGK- 59
MD +R +L+ AL VS+++ W D Q T +T A G GVPA G
Sbjct: 1 MDIKRTILIAALAVVSYVMVLKWNDDYGQAALPTQNTAASTVAPG--LPDGVPA GNGAS 58

Query: 60 -----LISVKTDVLDLTINTRGGDVEQALLPAYPKELNSTQ- 95
LI VKTDVL+L I+ GGD+ Q LP YP+ +
Sbjct: 59 ADVPSANAESSPAELAPVALSKDLIRVKTDVLELAIDPVGGDIVQLNLPKYPRRQDHPNI 118

Query: 96 PFQLLETSPQFIYQAQSGLTGRDGPDPNPANGPRPLYNVEKDAYVLAEGQNELQVPMTYTD 155
PFQL + + +Y AQSGLTG DGPD A+G RPLY E+ +Y LA+GQ +L V + ++D
Sbjct: 119 PFQLFDNGGERVYLAQSGLTGTDPDARASG-RPLYAAEQKSYQLADGQEQLVVDLKFSD 177

Query: 156 AAGNTFTKTFVLKRGDYAVNVNYNVQNAGEKPLEISSFGQLKQSITLPPHLDTGSSNFAL 215
N + K F KRG+Y +NV+Y + N + + F QLK+ + P T +
Sbjct: 178 NGVN-YIKRFSFKRGEYDLNVSYLIDNQSGQAWNGNMFAQLKRDASGDPSSSTATGTA-- 234

Query: 216 HTFRGAAYSTPDEKYEKYKFDTIADNENLNIS SKGGWVAMLQQYFATAWIPHNDGTNNFY 275
T+ GAA T E Y+K I D +L + GGWA LQ YF TAWIP N
Sbjct: 235 -TYLGAALWTASEPYKKVSMKDI-DKGS LKENVSGGWVAVLQHYFVTAWIPAKSDNNVVQ 292

Query: 276 TANLGNIAAIGYKSQPVLVQPGQTGAMNSTLWVGPEIQDKMAAVAPHLDTVDYGWLWF 335
T G IGY + V G ++ L+ GP+IQ K+ ++P L+LTV DYG+LWF
Sbjct: 293 TRKDSQGNIIIGYTGPVISVPAGGKVETSALLYAGPKIQSKLKE LSPGLELTVDYGFLWF 352

Query: 336 ISQPLFKLLKWIHSFVGNWGF SIIIIITFIVRGIMYPLTKAQYTSMAKMRMLQPKIQAMRE 395
I+QP+F LL+ IHS +GNWG+SII++T +++G+ +PL+ A Y SMA+MR + PK+ A++E
Sbjct: 353 IAQPIFWLLQHIHSL LGNWGWSIIIVLTMLIKGLFFPLSAASYRSMARMRAVAPKLAALKE 412

Query: 396 RLGD DKQRISQEMMALYKA EKV NPLGGCFPLLIQMPIFLALYMLMG SVELRQAPFALWI 455
R GDD+Q++SQ MM LYK EK+NPLGGC P+L+QMP+FLALY++L+ SVE+RQAP+ LWI
Sbjct: 413 RFGDDRQKMSQAMMELYKKEKINPLGGCLPILVQMPVFLALYWV LLESVEMRQAPWILWI 472

Query: 456 HDLSAQDPYYILPILMGVTMFFIQKMSPTTVDTPMQQKIMTFMPVIFTVFFLWFP SGLVL 515
DLS +DP++ILPI+MG TMF Q+++PT DPMQ K+M MP+IFT FFLWFP+GLVL
Sbjct: 473 TDSL IKDPFFILPIIMGATMFIQRLNPTP-PDPMQAKVMKMMPIIFTFFFLWFPAGLVL 531

Query: 516 YYIVSNLVTIIQQQLIYRGLE 536
Y++V+N ++I QQ I R +E
Sbjct: 532 YWVVNNCL SISQQWYITRRIE 552

>ref|ZP_00265074.1| COG0706: Preprotein translocase subunit YidC [Pseudomonas
fluorescens PfO-1]
Length = 560

Score = 467 bits (1202), Expect = e-130

Identities = 252/560 (45%), Positives = 346/560 (61%), Gaps = 32/560 (5%)

Query: 1 MDSQRNLLVIALLFVSFMIWQAWQDKNPQQAQQTQTOTTTTAAG----- 45
 MD +R +L++AL VS+++ W QD Q ++TT +G
 Sbjct: 1 MDIKRTILIVALAIVSYVMVLKWNQDYGQAALPTQNVASSTTSGLPDTATGNNAAASDD 60

Query: 46 ---SAADQGVPA-----SGQGKLISVKTDVLDLTINTRGGDVEQALLPAYPKELNSTQ-PF 97
 +A+D PA + LI +KTDVLDL+I+ +GGDV Q LP YP+ + PF
 Sbjct: 61 IPRAASDTSAPAETPVAASKDLIQIKTDVLDLSIDPQGGDVAQLTLPLYPRRQDRPDVPF 120

Query: 98 QLLETSPQFIYQAQSGLTGRDGPD-NPANGPRPLYNVEKDAYVLAEGQNELQVPMYTTDA 156
 QL + + Y AQSG L G +GPD NPA RP+Y+ EK Y LA+GQ++L V + ++
 Sbjct: 121 QLFNDGGERTYLAQSGLTGTNGPDANPAG--RPIYSSEKKTYQLADGQDKLVVDLKFSSK 178

Query: 157 AGNTFTKTFVLKRGDYAVNVNYNVQNAGEKPLEISSFGQLKQSITLPPHLDTGSSNFALH 216
 N + K F LKRG Y V V Y + N +P S F QLK+ + P T +
 Sbjct: 179 GVN-YIKRFTLKRGLYDVTVTYILIDNQAQPSWGSMAFLKRDASADPSSTTATGTA--- 234

Query: 217 TFRGAAYSTPDEKEYEKYKFDTIADNENLNISSEKGGWVAMLQQYFATAWIPHNDGTNNFYT 276
 T+ GAA T E Y+K + D L + GGWA LQ YF TAW+ N T
 Sbjct: 235 TYLGAALWTSSEPYKKVSMKDM-DKAQLKETVTGGWVAWLQHYFVTAWVAPKGENNIVQT 293

Query: 277 ANLGNGIAAIGYKSPVLVQPGQTAMNSTLWVGPEIQDKMAAVAPHLDLTVDYGWLWFI 336
 G IGY + PG ++ L+ GP+ Q + ++P L+LTVDYG LWFI
 Sbjct: 294 RKDSKGNYYIGYTGPSLTAAPGAKVETSAVLYAGPKSQAVLKELSPGLELTVDYGILWFI 353

Query: 337 SQPLFKLLKWIHSFVGNWGFSSIIITFIVRGIMYPLTKAQYTSMAKMRMLQPKIQAMRER 396
 +QP+F LL+ IHS VGNWG+SII +T +++GI +PL+ A Y SMA+MR + PK+ A++E+
 Sbjct: 354 AQPIFWLLQHIHSIVGNWGSIIIFLTMLIKGIFFPLSAASYKSMARMRAVAPKLAALKEQ 413

Query: 397 LGDDKQRISQEMMALYKAEKVNPLGGCFPLLIQMPIFLALYYMLMGSVELRQAPFALWIH 456
 GDD+Q++SQ MM LYK EK+NPLGGC P+L+QMP+FL+LY++L+ SVE+RQAPF LWI
 Sbjct: 414 HGDDRQKMSQAMMELYKKEKINPLGGCLPILVQMPVFLSLYWVLLESVEMRQAPFMLWIT 473

Query: 457 DLSAQDPYYILPILMGVTMFFIQKMSPTTVDPMQKIMTFMPVIFTVFFLWFPGLVLY 516
 DLS +DP++ILPI+MG TMF Q+++PT DPMQ K+M MP+IFT FFLWFP+GLVLY
 Sbjct: 474 DLSIKDPFFILPIIMGATMFIQQLNPTP-PDPMQAKVMKMMPIIFTFFFLWFPAGLVLY 532

Query: 517 YIVSNLVTIIQQQLIYRGLE 536
 ++V+N ++I QQ I R +E
 Sbjct: 533 WVVNNCLSLIAQQWYITRKIE 552

>ref|ZP_00124685.1| COG0706: Preprotein translocase subunit YidC [Pseudomonas syring
 pv. syringae B728a]
 Length = 563

Score = 461 bits (1187), Expect = e-129
 Identities = 247/562 (43%), Positives = 347/562 (61%), Gaps = 33/562 (5%)

Query: 1 MDSQRNLLVIALLFVSFMIWQAWQDKNPQQAQQTQTOTTTTAAG----- 45
 MD +R +L++AL V+++ W QD Q +TTA G
 Sbjct: 1 MDIKRTILIVALAIVTYVGVVLKWNQDYGQAAMPTQNVAASTTAPGIPDTAAGTNGSASAD 60

Query: 46 -----SAADQGVPAASGQGKLISVKTDVLDLTINTRGGDVEQALLPAYPKELNSTQ 95
 +AA PA LI VKTDVLDL I+ GGDV Q LP YP+ +
 Sbjct: 61 VPSANATANTAAAPLETPAVASKDLIHVKTDVLDLAI DPVGGDVVQLRLPLYPRRQDRPD 120

Query: 96 -PFQLLETSPQFIYQAQSGLTGRDGPDPNPANGPRPLYNVEKDAYVLAEGQNELQVPMYTT 154
 PFQL + + AQSG L G +GPD A G RP+Y + Y LA+GQ+ + V + ++
 Sbjct: 121 VPFQLFDNGGERTFLAQSGLTGTNGPDARAAG-RPVYTSTQKTYQLADGQDTMVVDLKF 179

Query: 155 DAAGNTFTKTFVLKRGDYAVNVNYNVQNAGEKPLEISSFGQLKQSITLPPHLDTGSSNFA 214
 + N + K F KRG Y + + Y V N +P + F QLK+ + P T +
 Sbjct: 180 ENGVN-YIKRFTFKRGLYDLVMTYVVDNQSAQPWSGNLFAQLKRDASSDPSSTTATGTA- 237

Query: 215 LHTFRGAAYSTPDEKEYEKYKFDTIADNENLNISSKGGWVAMLQQYFATAWIPHNDGTNNF 274
 T+ GAA T E Y+K I D + + +GGWVA LQ YF TAWIP ++ TN
 Sbjct: 238 --TYLGAALWTAAPYKKVSMKDI-DKGQVKETVQGGWVAWLQHYFVTAWIPDHNATNAV 294

Query: 275 YTANLNGIAAIGYKSQPVLVQPGQTGAMNSTLWVGPEIQDKMAAVAPHLDLTVDYGWLW 334
 T G IG+ S + V PG G ++TL+ GP+ Q + ++P L+LTVDYG+LW
 Sbjct: 295 QTRKDSQGNIIIGFTSPTLSVAPGAQGETSATLYAGPKSQAVLKELSPGLELTVDYGFLW 354

Query: 335 FISQPLFKLLKWIHSFVGNWGFSSIIITFIVRGIMYPLTKAQYTSMAKMRMLQPKIQAMR 394
 FI+QP+F LL+ IH+ +GNWG+SII++T +++G+ +PL+ A Y SMA+MR + PK+ ++
 Sbjct: 355 FIAQPIFWLLQHIHAILGNWGSIIIVLTMLIKGLFFPLSAASYKSMARMRAVAPKLALLK 414

Query: 395 ERLGDDKQRISQEMMALYKAEKVNPLGGCFPLLIQMPIFLALYYMLMGSVELRQAPFALW 454
 E+ GDD+Q++SQ MM LYK EK+NPLGGC P+L+QMP+FL+LY++L+ SVE+RQAP+ LW
 Sbjct: 415 EQHGDDRQKMSQAMMELYKKEKINPLGGCLPILVQMPVFLSLYWVLLESVEMRQAPWILW 474

Query: 455 IHDLSAQDPYYILPILMGVTMFFIQKMSPTTVTDPMQKIMTFMPVIFTVFFLWFPSGLV 514
 I DLS +DP++ILPI+MG TMF Q+++PT DPMQ K+M MP+IFT FFLWFP+GLV
 Sbjct: 475 ITDLSIKDPFFILPIIMGATMFIQRLNPTP-PDPMQAKVMKMMPIIFTFFFLWFEPAGLV 533

Query: 515 LYYIVSNLVTIIQQQLIYRGLE 536
 LY++V+N ++I QQ I R +E
 Sbjct: 534 LYWVVNNTLSIAQQAYITRKIE 555

>ref|NP_795330.1| inner membrane protein, 60 kDa [Pseudomonas syringae pv. tomato
 str. DC3000]
 Length = 562

Score = 460 bits (1184), Expect = e-128
 Identities = 246/558 (44%), Positives = 346/558 (62%), Gaps = 32/558 (5%)

Query: 1 MDSQRNLLVIALLFVSMIWAWEQDKNPQPAQQTQTTTTAAG----- 45
 MD +R +L++AL V+++ W QD Q + TA G
 Sbjct: 1 MDIKRTILIVALAIVTYVGVKWNQDYGQAAMPTQNVAASNTAPGIPDTAAGNNGSASAD 60

Query: 46 -----SAADQGV PASGQGLISVKTDVLDLTINTRGGDVEQALLPAYPKELNSTQ- 95
 SAA PA LI VKTDVLDL I+ GGDV Q LP YP+ +
 Sbjct: 61 VPSATGNTTSAAPLETFAVASKDLIHVKTDVLDLADIPVGGDVVQLRLPLYPRRQDRPDV 120

Query: 96 PFQLLETSPQFIYQAQSGLTGRDGPDPNANGPRPLYNVEKDAYVLAEGQNELQVPMYTYD 155
 PFQL + + + AQSGLTG +GPD A+G RP+Y+ + +Y LA+GQ+ + V + +++
 Sbjct: 121 PFQLFDNGGERTFLAQSGLTGTNGPDARASG-RPVYSSAQKSYQLADGQDSMVVELKFSE 179

Query: 156 AAGNTFTKTFVLKRGDYAVNVNYNVQNAGEKPLEISSFGQLKQSITLPPHLDTGSSNFAL 215
 N + K F KRG Y + + Y V N +P + F QLK+ + P T +
 Sbjct: 180 NGVN-YIKRFTFKRGLYDLVMTYVVDNQSAQPWAGNLFAQLKRDASSDPSSTTATGTA-- 236

Query: 216 HTFRGAAYSTPDEKEYEKYKFDTIADNENLNISSKGGWVAMLQQYFATAWIPHNDGTNNFY 275
 T+ GAA T E Y+K I D + + +GGWVA LQ YF TAWIP ++ TN
 Sbjct: 237 -TYLGAALWTAAPYKKVSMKDI-DKGQIKENVQGGWVAWLQHYFVTAWIPDHNVTNAVQ 294

Query: 276 TANLNGIAAIGYKSQPVLVQPGQTGAMNSTLWVGPEIQDKMAAVAPHLDLTVDYGWLWF 335
 T G IG+ S + V PG G +TL+ GP+ Q + ++P L+LTVDYG+LWF

Sbjct: 295 TRKDSQGNYYIIGFTSPTLSVAPGAQGETTATLYAGPKSQAVLKELSPGLELTVDYGFLWF 354

Query: 336 ISQPLFKLLKWIHSFVGNWGFSSIIITFIVRGIMYPLTKAQYTSMAKMRMLQPKIQAMRE 395
I+QP+F LL+ IH+ +GNWG+SII++T +++G+ +PL+ A Y SMA+MR + PK+ ++E

Sbjct: 355 IAQPIFWLLQHIHAILGNWGSIIIVLTMLIKGLFFPLSAASYKSMARMRAVAPKLAVLKE 414

Query: 396 RLGDDKQRISQEMMALYKAQKVNPLGGCFPLLIQMPIFLALYYMLMGSVELRQAPFALWI 455
+ GDD+Q++SQ MM LYK EK+NPLGGC P+L+QMP+FL+LY++L+ SVE+RQAP+ LWI

Sbjct: 415 QHGDDRQKMSQAMMELYKKEKINPLGGCLPILVQMPVFLSLYVWLLESVEMRQAPWILWI 474

Query: 456 HDLSAQDPYYILPILMGVTMFFIQKMSPTTVDTPMQQKIMTFMPVIFTVFFLWFP SGLVL 515
DLS +DP++ILPI+MG TMF Q+++PT DPMQ K+M MP+IFT FFLWFP+GLVL

Sbjct: 475 TDSLKDPFFILPIIMGATMFIQRLNPTP-PDPMQAKVMKMMPIIFTFFFLWFPAGLVL 533

Query: 516 YYIVSNLVTIIQQQLIYR 533
Y++V+N ++I QQ I R

Sbjct: 534 YWVNNNTLSIAQQAYITR 551

>ref|ZP_00140404.2| COG0706: Preprotein translocase subunit YidC [Pseudomonas
aeruginosa UCBPP-PA14]
Length = 578

Score = 446 bits (1147), Expect = e-124

Identities = 248/579 (42%), Positives = 345/579 (59%), Gaps = 50/579 (8%)

Query: 1 MDSQRNLLVIALLFVSFMIWQAWEQDKNPQ-----PQAQOTTQT TTTT 42
MD QR++L++AL VS+++ W +D P A T+ T

Sbjct: 1 MDIQRSILIVALAVVSYLLVLQWNKDYGQPELPAASAMNTTQGLPDTSPASGTSSDVPT 60

Query: 43 AAGSAADQGV---PASGQGKLISVKT DVLDLTINTRGGDVEQALLPAYPKELNSTQ-PFQ 98
A SAA P + KLI VKTDVLDL I+ RGGD+ Q L YP+ L+ PF

Sbjct: 61 AQSSAAGSEAADKPVAVSDKLIQVKT DVLDLAIDPRGGDIVQLGLLQYPRRLDRPDVPFP 120

Query: 99 LLETSPQFIYQAQSGLTGRDGPDPNPANGPRPLYNVEKDAYVLAEGQNELQVPMTYTDAAG 158
L + + Y AQSGLTG DGPD + G RPL++ + +Y LA+GQNEL V ++++

Sbjct: 121 LFDNGRERTYLAQSGLTGADGPDASSAG-RPLFHSQAQSSYQLADGQNELVVDLSFSHDGV 179

Query: 159 NTFTKTFVLKRG-----DYAVNVNYNVQNAGEKPLEISSFGQLK 197
N + K F RG Y V V+Y + N K + F QLK

Sbjct: 180 N-YIKRFTFHRGLKADCSDKEKAQKKIECINENAYQGVSYLIDNQSGKTWSGNLFAQLK 238

Query: 198 QSITLPPHLDTGSSNFALHTFRGAAYSTPDEKYEKYKFDTIADNENLNIS SKGGWVAMLQ 257
+ + P T + + T+ GAA TPD Y+K + D E S +GGWVA LQ

Sbjct: 239 RDGSADPSSTTATG---VSTYLGAAVWTPDSPYKKISTKDM-DKEQFKESVQGGWVAWLQ 294

Query: 258 QYFATAWIPHNDGTNNFYTANLGNIAAIGYKSQPVLVQPGQTGAMNSTLWVGPEIQDKM 317
YF TAW+P + T G G +G+ + V G + TL+ GP++Q +

Sbjct: 295 HYFVTAWVP TKGEQHQMTRKDGQGNYYIVGFTGPTLSVPAGSKVETDLTLYAGPKLQKHL 354

Query: 318 AAVAPHLDLTVDYGWLWFISQPLFKLLKWIHSFVGNWGFSSIIITFIVRGIMYPLTKAQY 377
++P L+LTVDYG+LWFI+QP+F LL+ IHS +GNWG+SII +T +++ +PL+ A Y

Sbjct: 355 KELSPGLELTVDYGFLWFIAQPIFWLLQHIHSLIGNWGSIIALT VLIKLAFFPLSAASY 414

Query: 378 TSMKMRMLQPKIQAMRERLGDDKQRISQEMMALYKAQKVNPLGGCFPLLIQMPIFLALY 437
SMA+MR + PK+QA++E+ GDD+Q++SQ MM LYK EK+NPLGGC P+L+QMP+FL+LY

Sbjct: 415 RSMARMRAVSPKMQAIKEQHGDDRQKMSQAMMELYKKEKINPLGGCLPILVQMPVFLSLY 474

Query: 438 YMLMGSVELRQAPFALWIHDLAQDPYYILPILMGVTMFFIQKMSPTTVDTPMQQKIMTF 497

++L+ SVE+RQAP+ WI DLS +DP++ILPI+MG TM Q ++PT DPMQ K+M
 Sbjct: 475 WVLESVEMRQAPWLGWITDLSVKDPFFILPIVMGGTMLIQQMLNPTP-PDPMQAKVMKL 533

Query: 498 MPVIFTVFFLWFP SGLVLYYIVSNLVTIIQQQLIYRGLE 536
 MP+IFT FFLWFP+GLVLY++V+N ++I QQ I R +E
 Sbjct: 534 MPIIFTFFFLWFPAGLVLYWVNNCL SIAQQWYITRKIE 572

>ref|NP_254255.1| hypothetical protein PA5568 [Pseudomonas aeruginosa PAO1]
 Length = 578

Score = 446 bits (1146), Expect = e-124
 Identities = 248/579 (42%), Positives = 344/579 (59%), Gaps = 50/579 (8%)

Query: 1 MDSQRNLLVIALLFVSMIWAWEQDKNPQ-----PQAQQTQTQTTT 42
 MD QR++L++AL VS+++ W +D P A T+ T
 Sbjct: 1 MDIQRSILIVALAVVS YLLVLQWNKDYGQPELPAASASMNTTQGLPDTSPASGTSSDVPT 60

Query: 43 AAGSAADQGV---PASGQGKLISVKT DVLDTINTRGGDVEQALLPAYPKELNSTQ-PFQ 98
 A SAA P + KLI VKTDVLDL I+ RGGD+ Q L YP+ L+ PF
 Sbjct: 61 AQSSAAGSEAADKPVAVSDKLIQVKT DVLDLAIDPRGGDIVQLGLLQYPRRLDRPDVPFP 120

Query: 99 LLETSPQFIYQAQSGLTGRDGPDPNPANGPRPLYNVEKDAYVLAEGQNELQVPMTYTDAAG 158
 L + + Y AQSGLTG DGPD + G RPL+ + +Y LA+GQNEL V ++++
 Sbjct: 121 LFDNGRERTYLAQSGLTGADGPDASSAG-RPLFRSAQSSYQLADGQNELVVDLSFSHDGV 179

Query: 159 NTFTKT FVLKRG-----DYAVNVNINVQNAGEKPLEISSFGQLK 197
 N + K F RG Y V V+Y + N K + F QLK
 Sbjct: 180 N-YIKRFTFHRGLKADCSDKEKAQKKIECINENAYQGVSYLIDNQSGKTWSGNLFAQLK 238

Query: 198 QSITLPPHLD TGSSNFALHTFRGAAYSTPDEKYEKYKFDTIADNENLNIS SKGGWVAMLQ 257
 + + P T + + T+ GAA TPD Y+K + D E S +GGWA LQ
 Sbjct: 239 RDGSADPSSTTATG---VSTYLGA AVWTPDSPYKKISTKDM-DKEQFKESVQGGWVAWLQ 294

Query: 258 QYFATAWIPHNDGTNNFYTANLGNIAAIGYKSQPVLVQPGQTGAMNSTLWVGPEIQDKM 317
 YF TAW+P + T G G +G+ + V G + TL+ GP++Q +
 Sbjct: 295 HYFVTAWVP TKGEQHQMTRKDGQGNYIVGFTGPTLSVPAGSKVETDLTLYAGPKLQKHL 354

Query: 318 AAVAPHLDLTVDYGWLWFISQPLFKLLKWIHSFVGNWGF SIIIIITFIVRGIMYPLTKAQY 377
 ++P L+LTVDYG+LWFI+QP+F LL+ IHS +GNWG+SII +T +++ +PL+ A Y
 Sbjct: 355 KELSPGLELTVDYGFLWFIAQPIFWLLQHIHSLIGNWGSIIALT VLIKLAFFPLSAASY 414

Query: 378 TSMAMRMLQPKIQAMRERLGDDKQRISQEMMALYKA EKVNPLGGCFPLLIQMPIFLALY 437
 SMA+MR + PK+QA++E+ GDD+Q++SQ MM LYK EK+NPLGGC P+L+QMP+FL+LY
 Sbjct: 415 RSMARMRAVSPKMQAIKEQHGD DRQMSQAMMELYKKEKINPLGGCLPILVQMPVFLSLY 474

Query: 438 YMLMG SVELRQAPFALWIHDL SAQDPYI LPILMGVTMFFIQKMSPTTVTDPMQOKIMTF 497
 ++L+ SVE+RQAP+ WI DLS +DP++ILPI+MG TM Q ++PT DPMQ K+M
 Sbjct: 475 WVLESVEMRQAPWLGWITDLSVKDPFFILPIVMGGTMLIQQMLNPTP-PDPMQAKVMKL 533

Query: 498 MPVIFTVFFLWFP SGLVLYYIVSNLVTIIQQQLIYRGLE 536
 MP+IFT FFLWFP+GLVLY++V+N ++I QQ I R +E
 Sbjct: 534 MPIIFTFFFLWFPAGLVLYWVNNCL SIAQQWYITRKIE 572

>ref|YP_115424.1| inner membrane protein, 60 kDa [Methylococcus capsulatus str. Bath]
 Length = 545

Score = 429 bits (1104), Expect = e-119

Identities = 223/550 (40%), Positives = 338/550 (61%), Gaps = 23/550 (4%)

Query: 1 MDSQRNLLVIALLFVSFMIWQAWQDKNPQQAQQTQTOTTTTAAGSAADQG----- 51
 MD+ R +L + +F+SF++W+ W+ D P+PQA T + AG +
 Sbjct: 1 MDNLRFLVLFVFFIFLSFLLWEQWQIDYGPQPQAVAQTDGASRPAGDLPQRPSDDSDVTV 60

Query: 52 ---VPASGQGKLISVKTDVLDLTINTRGGDVEQALLPAYP-KELNSTQPFQQLLETSPQFI 107
 P + I V TDVL L I+TRGGD+ Q L YP + +P+LL T I
 Sbjct: 61 HTEAPTQEGSRRIRVHTDVLSEIDTRGGDLRQLDLLNYPVSKEQPDRPVRLL-TDQGD I 119

Query: 108 YQAQSGLTGRDGPDPNPANGPRPLYNVEKDAYVLAEGQNELQVPMTYTDAAGNTFTKTFVL 167
 + AQSG G L+ E Y L +GQ+ L+VP+T++D G T TKT++L
 Sbjct: 120 FVAQSGFIGAA---QQVFNHSLWQAEAGEYRLQDGDILRVPLTWSQGQVTVTKTYIL 176

Query: 168 KRGDYAVNVNYNVNQNAKEKPLEISSFGQLKQSITLPPHLDTGSSNFALHTFRGAAYSTPD 227
 +RG Y +++ + N + QL++ P S F + T+ G T D
 Sbjct: 177 RRGSYLIDMEQTIDNRSNTNWTGRQYMLQQRK---EPTSAQEDSQF-IRTYTGGVLHTED 232

Query: 228 EKYEKYKFDTIADNENLNISSKGGWVAMLQOYFATAWIPHNDGTNNFYTANLGNIAAIG 287
 + YEK F +A NL+ S+ GW+AM+Q YF AW+P + + FYT L + + IG
 Sbjct: 233 KSYEKIAFKDMASG-NLDAKSRQGWIAMIQHYFLAAWVPPAEDESTFYTKALADRVFVIG 291

Query: 288 YKSQPVLVQPGQGTGAMNSTLWVGPEIQDKMAAVAPHLDLTVDYGWLWFISQPLFKLLKWI 347
 S P V G + + + L+ GP++Q + +AP L+LT D+G L I++P++ LL+
 Sbjct: 292 AYSPPAEVPAGSSQTLKARLFAGPKLQHVLEGIAPGLELTADFGILTVIAPKIYWLLETF 351

Query: 348 HSFVGNWGFSSIIITFIVRGIMYPLTKAQYTSMAKMRMLQPKIQAMRERLGDDKQRISQE 407
 H F NWG++II +T +++ + + L++A Y SMA MR LQPK+ ++ER G+D+QR +Q
 Sbjct: 352 HGFFNNWGWAIIFVTLVIKALFFKLSEASYRSMANMRKLQPKLVELKERYGEDRQRYNQA 411

Query: 408 MMALYKAQKVNPLGGCFPLLIQMPIFLALYYMLMGSVELRQAPFALWIHDLQAQDPYYIL 467
 MM LY+ EKVNPLGGC P+L+Q+P+F++LY++L+ SV+LRQAPF LW+ DLS++DPY++L
 Sbjct: 412 MMELYRKEKVNPLGGCLPILVQIPVFISLYWVLVESVDLRQAPFLLWLDDLSSKDPYFVL 471

Query: 468 PILMGVTMFFIQKMSPTTVDTPMQQKIMTFMPVIFTVFFLWFPGLVLYYIVSNLVTTIIQ 527
 P++MGV+MF Q+++P TDP+Q ++M F P++FTVFFL+FPSGLVLY++V+N+++IIQ
 Sbjct: 472 PLIMGVSMFIQQLNPPP-TDPIQARVMQFFPLVFTVFFLFFPSGLVLYWVNNILSIIQ 530

Query: 528 QQLIYRGLEK 537
 Q I R +EK
 Sbjct: 531 QWYITRQIEK 540

>ref|ZP_00145659.2| COG0706: Preprotein translocase subunit YidC [Psychrobacter sp.
 273-4]

Length = 565

Score = 428 bits (1101), Expect = e-119

Identities = 238/559 (42%), Positives = 343/559 (61%), Gaps = 36/559 (6%)

Query: 5 RNLLVIALLFVSFMIWQAWQDKNPQQAQQTQTOTTTTA-----AGSAADQGV----- 52
 R +++IA+L ++++ AW D P +T T+ +G+A D V
 Sbjct: 6 RVMIIIIAMLITAYLLILAWRDDYADAPAVDTPPETATSVGADIPSTSGAAGDIPVQTLPV 65

Query: 53 -----PASGQGKLISVKTDVLDLTINTRGGDVEQALLPAYPKELNSTQPFQL 99
 PA+ G LI+V TD D+ IN GGD+ A L Y L+S +PF L
 Sbjct: 66 DNGTVDNSAVTATPATDAG-LITVTTDRYDIKINPEGGDIVYAALKQYDATLSDSKPFVL 124

Query: 100 LETSPQFIYQAQSGLTGRDGPDPNPANGPRPLYNVEKDAYVLAEGQNELQVPMTYTDAGN 159
 LE + +Y AQSG L G++G D A G R Y+ + YV+ +GQ L VP+TY G
 Sbjct: 125 LENNSNRVYVAQSG LIGQNGIDT-AEG-RAKYSHTANNYVMEKGQQTLSVPLTYKKD-GV 181

Query: 160 TFTKTFVLKRGDYAVNVNYNVQNAAGEKPLEISSFGQLKQSITLPPHL-DTGSSNFALHTF 218
 T TKTF Y ++++Y +QNA + F QLK+ + P + D G+ + A T+
 Sbjct: 182 TITKTFSTHDKYPIDISYKIQNASTAAWQGMFAQLKRDDSKDPGMSDKGALSMA--TY 239

Query: 219 RGAAYSTPDEKYEKYKFDTIADNENLNISSKGGWVAMLQQYFATAWIPHNDGTNNFYTAN 278
 G A+ TPD+ Y K KF D E L +S GWV ++Q YF +AW P N T F++
 Sbjct: 240 LGGAWGTPDDPYNKLKFGNFNDGE-LTTTSDKGWVGIVQHYFVSAWTPENF-TGKFFSRE 297

Query: 279 LGNGIAAIGYKSQPVLVQPGQTGAMNSTLWVGPEIQDKMAAVAPHLDLTVDYGLWLFISQ 338
 G+ IG+ SQPV V P + +N+TL+ GP++Q ++ VA L+ TVDYG LW IS+
 Sbjct: 298 TGDDYF-IGFNSQPVNVAPDKQVTLNATLYAGPKVQSELKDVAAGLNQTVDYGLLWPISK 356

Query: 339 PLFKLLKWIHSFVGNWGFSSIIITFIVRGIMYPLTKAQYTSMAKMRMLQPKIQAMRERLG 398
 LF LL IH +GNWG+SII++T +V+ + + Y SMAKMR + P++ A++E G
 Sbjct: 357 ILFALLDGIHKIIGNWGWSSIILLTILVKFALMWFSNKSYYSMKMRAPRLAALKEEHG 416

Query: 399 DDKQRISQEMMALYKAEKVNPLGGCFPLLIQMPIFLALYMLMGVSVELRQAPFALWIHDL 458
 DD+ ++SQEMMA+YK EKVNP+ GC P+L+QMPIFLALY++L+ S+ELR AP+ LWI DL
 Sbjct: 417 DDRMKMSQEMMAMYKEEKVNPMAGCLPILMQMPIFLALYWVLVESIELRHAPVWLWIQDL 476

Query: 459 SAQDPYYILPILMGVTMFFIQKMSPTTVDPMQQKIMTFMPVIFTVFFLWFPSGLVLYYI 518
 SA DP++ILP+LMGV+MF Q+++P DPMQ K+M F+P+IFT F L+FP+GLVLY+
 Sbjct: 477 SAMDPWFILPLLMGVSMFVQQQLNPQP-ADPMQAKVMKFLPIIFTAFMLFFPAGLVLYWT 535

Query: 519 VSNLVTIIQQQLIYRGLEK 537
 V+NL ++ Q ++ + +E+
 Sbjct: 536 VNNLFSMTHQYIVNKKVEE 554

>ref|YP_125376.1| hypothetical protein lpp3074 [Legionella pneumophila str. Paris]
 Length = 556

Score = 427 bits (1098), Expect = e-118

Identities = 232/552 (42%), Positives = 332/552 (60%), Gaps = 31/552 (5%)

Query: 1 MDSQRNLLVIALLFVSFMIWQAWEQDKNPQPAQQTQTQTTTAAAGSAADQGV----- 53
 MD +R +L +AL + +W AW+ D + ++ T + T+ G Q +P
 Sbjct: 1 MDIRRVLYMALALIGLSLWNAWQIDYPAKQPVEEKTASQLTSDGHLLPQIIPSNAEQPI 60

Query: 54 -----ASGQGKLISVKTDVLDLTINTRGGDVEQALLPAYPKEL-NSTQPFQLLETSPQ 105
 AS +LI VKTDVLD+ I+ + GD+ + LL YP + + +PF LL+
 Sbjct: 61 TLKAEKASSSKQLIQVKTDVLDVLDIDLKNQDIVKGLLLDYPLSVEDKNKPFLLQNQAS 120

Query: 106 FIYQAQSGLTGRDGPDPNPANGPRPL---YNVEKDAYVLAEGQNELQVPMTYTDAGNTFT 162
 Y A S L DG P+ L + EK+ Y L QN+L V + G
 Sbjct: 121 QRYVANSSLFILDGQT-----PQSLDFDFTSEKEYYELKSDQNQLIVTLNGKSEDGLDVK 175

Query: 163 KTFVLKRGDYAVNVNYNVQNAAGEKPLEISSFGQLKQSITLPPHLDTGSSNFALHTFRGAA 222
 K FV +G Y + VNY + N G + G + + SS F + ++ GA+
 Sbjct: 176 KEFVFTKGSYLIEVNYKIANGTNSLWK----GYFNTQLLRSSPKEDKSSIFHIGSYTGAS 231

Query: 223 YSTPDE-KYEKYKFDTIADNENLNISSKGGWVAMLQQYFATAWIPHNDGTNNFYTANLGN 281
 +S P + +Y+K F ++ + NL++ +KGGW+AM Q YF +AW+P+ D N FYT
 Sbjct: 232 FSNPGKNRYQKVSFSDMSKS-NLDVDAKGGWIAMQQHYFLSAWVPNADSENKFYTLATDK 290

Query: 282 GIAAIGYKSQPVLVQPGQTGAMNSTLWVGPEIQDKMAAVAPHLDLTVDYGWLWFISQPLF 341
IG SQP+ V+P + + S L++GPEI + ++P LDLTVDYG LWF+S LF
Sbjct: 291 DYT-IGAVSQPITVKPKEDKIVGSKLYIGPEITSVLKGISPSLDLTVDYGILWFLSSLLF 349

Query: 342 KLLKWIHSFVGNWGFSSIIITFIVRGIMYPLTKAQYTSMAKMRMLQPKIQAMRERLGDDK 401
L+K I++ VGNWG+SI+++T +++ Y L+ Y SMA MR LQPK+QA+RER GDDK
Sbjct: 350 SLMKAIYTVVGNWGSIVLVTVLIKLAFYRLSATSYSKMASMRKLQPKLQALRERYGDDK 409

Query: 402 QRISQEMMALYKAEKVNPLGGCFPLLIQMPIFLALYYMLMGSVELRQAPFALWIHDLASAQ 461
+ISQ M LYK EKNVPLGGC P+LIQ+P+F+ALY++L+ SVELRQAPF WI+DL++
Sbjct: 410 AKISQATMELYKQEKVNPLGGCLPILIQIPVFIALYWVLLESVELRQAPFIFWINDLASA 469

Query: 462 DPYYILPILMGVTMFFIQKMSPTTVDTPMQQKIMTFMPVIFTVFFLWFPGLVLYYIVSN 521
DPY++LP++MG TM QK++P DPMQ K+M F+P++FT F FPSGLVLY+IV+N
Sbjct: 470 DPYHVLPLIMGATMLIQKLNPA-ADPMQAKVMMFLPILFTGLFWNFPSGLVLYWIVNN 528

Query: 522 LVTIIQQQLIYR 533
++I+QQ I R
Sbjct: 529 TLSILQQWYITR 540

>ref|YP_096994.1| inner membrane protein, 60 kDa [Legionella pneumophila subsp.
pneumophila str. Philadelphia 1]
Length = 556

Score = 426 bits (1096), Expect = e-118
Identities = 232/552 (42%), Positives = 332/552 (60%), Gaps = 31/552 (5%)

Query: 1 MDSQRNLLVIALLFVSMIWAWEQDKNPQQAQQTQTTTTAAGSAADQGPV----- 53
MD +R +L +AL + +W AW+ D + ++ T + T+ G Q +P
Sbjct: 1 MDIRRIVLYMALALIGLSLWNAWQIDYPAKQPVEEKTASQLTSDGHLLPQIIPSNAEQPV 60

Query: 54 -----ASGQGLISVKTDVLDLTINTRGGDVEQALLPAYPKEL-NSTQPFQLETSPQ 105
AS +LI VKTDVLD+ I+ + GD+ + LL YP + + +PF LL+
Sbjct: 61 TLKAEKASSGKQLIQVKTVDLVDIDLKNGDIVKGLLLDYPLSVEDKNKPFLLQNQAS 120

Query: 106 FIYQAQSGLTGRDGPDPNPANGPRPL---YNVEKDAYVLAEGQNELQVPMTYTDAAGNTFT 162
Y A S L DG P+ L + EK+ Y L QN+L V + G
Sbjct: 121 QRYVANSSLFVLDGQT-----PQSLDFDFTSEKEYYELKPDQNQLIVTLNGKSEDGLDVK 175

Query: 163 KTFVLKRGDYAVNVNYNVQNAGEKPLEISSFGQLKQSITLPPHLDTGSSNFALHTFRGAA 222
K FV +G Y + VNY + N G + G + + SS F + ++ GA+
Sbjct: 176 KEFVFTKGSYLIEVNYKIAN TGNSLWK----GYFNTQLLRSSPKEDKSSIFHIGSYTGAS 231

Query: 223 YSTPDE-KYEKYKFDTIADNENLNISSKGGWVAMLQQYFATAWIPHNDGTNNFYTANLGN 281
+S P + +Y+K F ++ + NL++ +KGGW+AM Q YF +AW+P+ D N FYT
Sbjct: 232 FSNPGKNRYQKVSFSDMSKS-NLDVDAKGGWIAMQQHYFLSAWVPNADSENKFYTLATDK 290

Query: 282 GIAAIGYKSQPVLVQPGQTGAMNSTLWVGPEIQDKMAAVAPHLDLTVDYGWLWFISQPLF 341
IG SQP+ V+P + + S L++GPEI + ++P LDLTVDYG LWF+S LF
Sbjct: 291 DYT-IGAVSQPITVKPKEDKIVGSKLYIGPEITSVLKGISPSLDLTVDYGILWFLSSLLF 349

Query: 342 KLLKWIHSFVGNWGFSSIIITFIVRGIMYPLTKAQYTSMAKMRMLQPKIQAMRERLGDDK 401
L+K I++ VGNWG+SI+++T +++ Y L+ Y SMA MR LQPK+QA+RER GDDK
Sbjct: 350 SLMKAIYTVVGNWGSIVLVTVLIKLAFYRLSATSYSKMASMRKLQPKLQALRERYGDDK 409

Query: 402 QRISQEMMALYKAEKVNPLGGCFPLLIQMPIFLALYYMLMGSVELRQAPFALWIHDLASAQ 461
+ISQ M LYK EKNVPLGGC P+LIQ+P+F+ALY++L+ SVELRQAPF WI+DL++
Sbjct: 410 AKISQATMELYKQEKVNPLGGCLPILIQIPVFIALYWVLLESVELRQAPFIFWINDLASA 469

Query: 462 DPYYILPILMGVTMFFIQKMSPTTVDPMQKIMTFMPVIFTVFFLWFPSGLVLYIYVSN 521
 DPY++LP++MG TM QK++P DPMQ K+M F+P++FT F FPSGLVLY+IV+N
 Sbjct: 470 DPYHVLPLIMGATMLIQKLNPA-ADPMQAKVMMFLPIFLTGLFWNFPSGLVLYWIVNN 528

Query: 522 LVTIIQQQLIYR 533
 ++I+QQ I R
 Sbjct: 529 TLSILQQWYITR 540

>ref|NP_820897.1| inner-membrane protein, 60kDa [Coxiella burnetii RSA 493]
 Length = 566

Score = 426 bits (1095), Expect = e-118
 Identities = 233/575 (40%), Positives = 349/575 (60%), Gaps = 40/575 (6%)

Query: 1 MDSQRNLLVIALLFVSMIWAWEQDKNPQQAQQTQTOTTTAAGSAADQGPASGQG-- 58
 MD +R +L + + ++ ++ AW++D P P+ T + T PA G
 Sbjct: 1 MDIKRIILYVIVALLAIALFNAWQRDYPPTPKPTPTVEQPTANGDHPATYTPPAFTPGAA 60

Query: 59 -----KLISVKTDVLDLTINTRGGDVEQALLPAYPKELNSTQ-PFQL 99
 +LI+V+TDVLD+ I+T+GG++ A LP YP L Q P Q+
 Sbjct: 61 EKTKKAGTIAFTSKVPEARLITVRTDVLDVEIDTQGGNIVSAKLPKYPVSLEEKQTPVQI 120

Query: 100 LETSPQFIYQAQSGLTGRDGPDPNPANGPRPLYNVEKDAYVLAEGQNELQVPMTYTDAAGN 159
 L P +Y AQSGLT +G + EK YVL GQN+L V +T G
 Sbjct: 121 LSGEPNELYIAQSGLTNGNGQPTTVQ-----FESEKKQYVLENGQNQLIVQLTGRAPDGL 175

Query: 160 TFTKTFVLKRGDYAVNVNYNVQNAGEKPLEISSFGQLKQSITLPPHLDTGSSNFALHTFR 219
 TKT+ R DYA+++ Y V+N KP + S + Q+ + PP T +F + ++
 Sbjct: 176 LVTKTYTFHRDDYAIHLAYQVKNNSTKWPQGSlytQITRR--QPP---TEHHHFYVRSYN 230

Query: 220 GAAYSTPDEKYEKFKFDTIADNENLNISKGGWVAMLQQYFATAWIPHN-DGTNNFYT-- 276
 GA+ +P YEK ++++ D +N++ +S+ GW+AM Q YF +AW+P N + T ++Y+
 Sbjct: 231 GASMGSPQTPYEKLSYESL-DKQNIIDRTSQSGWIAMQQHYFLSAWVPGNPELTYHYSHV 289

Query: 277 --ANLNGIAAIGYKSQPVLVQPGQTGAMNSTLWVGPEIQDKMAAVAPHLDLTVDYGWLW 334
 A+ + +G+ S + V G A ++TL+VGPEI ++ +AP L+ T+DYGWLW
 Sbjct: 290 IPASDEPNVYVGVFVSPQMNVAAGSEAATHATLYVGPEIAKRLKGLAPGLERTIDYGWLW 349

Query: 335 FISQPLFKLLKWIHSFVGNWGFSSIIITFIVRGIMYPLTKAQYTSMAKMRMLQPKIQAMR 394
 IS LF +L +H+ V NWG+SIII T +++ + Y + + SMA+MR +QP+IQ++
 Sbjct: 350 PISMLLFWILSAVHAVVKNWGSIIITILIKIVFYWFSKSFRRSMARMREMOPRIQALK 409

Query: 395 ERLGDDKQRISQEMMALYKAQKVNPLGGCFPLLIQMPIFLALYYMLMGSVLRQAPFALW 454
 ER GDD+Q +S+ M LY+ EK+NPLGGC P+LIQ+P+F+A YY+++ SV+LRQAPF W
 Sbjct: 410 ERHGDDRQALSRTMELRKEKINPLGGCLPMLIQVPVFIAFYVYIIESVQLRQAPFIW 469

Query: 455 IHDLSAQDPYYILPILMGVTMFFIQKMSPTTVDPMQKIMTFMPVIFTVFFLWFPSGLV 514
 IHDLS +DPYYILPI+MG++M Q +SPT+ DP QQK+M +PVIFTVFF+ FP+GLV
 Sbjct: 470 IHDLSVKDPYYILPIIMGLSMLAQQWVSPTS-PDPTQQKMMWILPVIFTVFFINFAPGLV 528

Query: 515 LYYIVSNLVTIIQQQLIYRGLE--KRGLHSREKKK 547
 LY+I +N+V +QQ + + E K L +R +K
 Sbjct: 529 LYWITNNVVQTLQQWYVKNKYTESHKAKLKARRARK 563

>ref|YP_128254.1| hypothetical protein lpl2930 [Legionella pneumophila str. Lens]

Length = 556

Score = 426 bits (1094), Expect = e-118

Identities = 231/552 (41%), Positives = 332/552 (60%), Gaps = 31/552 (5%)

Query: 1 MDSQRNLLVIALLFVSFMIWQAWQDKNPQPQAQQTQTTTTAAGSAADQGV----- 53
 MD +R +L +AL + +W AW+ D + ++ T + T+ G Q +P
 Sbjct: 1 MDIRRVLYMALALIGLSLWNAWQIDYPAKQPVEEKTASQLTSDGHLLPQIIPSNAEQPV 60

Query: 54 -----ASGQGKLIQVKTDLVLDLTINTRGGDVEQALLPAYPKEL-NSTQPFQLLETSPQ 105
 AS +LI VKTD+LD+ I+ + GD+ + LL YP + + +PF LL+
 Sbjct: 61 TLKAEKASSGKQLIQVKTDLVDIDLKNGDIVKGLLLDYPLSVEDKNKPFLLQNQAS 120

Query: 106 FIYQAQSGLTGRDGPDPNPANGPRPL---YNVEKDAYVLAEGQNELQVPMYTYTDAAGNTFT 162
 Y A S L DG P+ L + EK+ Y L QN+L V + G
 Sbjct: 121 QRYVANSSLFVLDGQT-----PQSLDFDFTSEKEYYELKPDQNQLIVTLNGKSEDGLDVK 175

Query: 163 KTFVLKRGDYAVNVNYNVQNAAGEKPLEISSFGQLKQSITLPPHLDTGSSNFALHTFRGAA 222
 K FV +G Y + VNY + N G + G + + SS F + ++ GA+
 Sbjct: 176 KEFVFTKGSYLIEVNYKIANIGNSLWK----GYFNTQLLRSSPKEDKSSIFHIGSYTGAS 231

Query: 223 YSTPDE-KYEKYKFDTIADNENLNISSEKGGWVAMLQQYFATAWIPHNDGTNNFYTANLGN 281
 +S P + +Y+K F ++ + NL++ +KGGW+AM Q YF +AW+P+ D N FYT
 Sbjct: 232 FSNPGKNRYQKVSFSDMSKS-NLDVDAKGGWIAMQQHYFLSAWVPNADSENKFYTLATDK 290

Query: 282 GIAAIGYKSQPVLVQPGQTGAMNSTLWVGPEIQDKMAAVAPHLDLTVDYGWLWLFISQPLF 341
 IG SQP+ V+P + + S L++GPEI + ++P LDLTVDYG LWF+S LF
 Sbjct: 291 DYT-IGAVSQPITVKPKEDKIVGSKLYIGPEITSVLKGISPSLDLTVDYGILWFLSSLLF 349

Query: 342 KLLKWIHSFVGNWGFSSIIITFIVRGIMYPLTKAQYTSMAKMRMLQPKIQAMRERLGDDK 401
 L+K I++ VGNWG+SI+++T +++ Y L+ Y SMA MR LQPK+QA+RER GDDK
 Sbjct: 350 SLMKAIYTVVGNWGSIVLVTVLIKLAFLYRLSATSYSKMSMRKLQPKLQALRERYGDDK 409

Query: 402 QRISQEMMALYKAQKVNPLGGCFPLLIQMPIFLALYMLMGSVELRQAPFALWIHDLSAQ 461
 +ISQ M LYK EKNVPLGGC P+LIQ+P+F+ALY++L+ SVELRQAPF WI+DL++
 Sbjct: 410 AKISQATMELYKQEKVNPLGGCLPILIQIPVFIALYWVLLESVELRQAPFIFWINDLASA 469

Query: 462 DPYYILPILMGVTMFFIIQKMSPTTVDTPMQQKIMTFMPVIFTVFFLWFPGLVLYYIVSN 521
 DPY++LP++MG TM QK++P DPMQ K+M F+P++FT F FPSGLVLY+IV+N
 Sbjct: 470 DPYHVLPLIMGATMLIQKLNPA-ADPMQAKVMMFLPILFTGLFWNFPSGLVLYWIVNN 528

Query: 522 LVTIIQQQLIYR 533
 ++I+QQ I R
 Sbjct: 529 TLSILQQWYITR 540

>ref|ZP_00350183.1| COG0706: Preprotein translocase subunit YidC [Methylobacillus
 flagellatus KT]
 Length = 552

Score = 418 bits (1074), Expect = e-116

Identities = 217/554 (39%), Positives = 340/554 (61%), Gaps = 30/554 (5%)

Query: 1 MDSQRNLLVIALLFVSFMIWQAWQDKNPQPQAQ-QTT-----QTTTTAAGSAAD 49
 MD++R +L + F M+W +W++D+ P +Q QTT Q ++A +A
 Sbjct: 1 MDTKRLILFVIFSILMLWDSWQRDQPPAASQTQTTAQSVEDGSVPQAASASAANQ 60

Query: 50 QGVPAQSGQKL-----ISVKTDLVLDLTINTRGGDVEQALLPAYPKELNSTQPFQLLET-S 103
 VPA +L I+V+TD+ +I+T GGD+ + L + + + T+ F L++ S

Sbjct: 61 ASVPAETGFRLQSAERINVEDLYKASIDTIGGDLRRLELREHKDDDEDQTKNFVLMDDQS 120

Query: 104 PQFIYQAQSGLTGRDGPDPNPANGPRPLYNVEKDAYVLAEGQNELQVPMTYTDAAGNTFTK 163
 +Y AQ+GL G P + + ++ E Y LA G+++L V +T+ G K

Sbjct: 121 APMLYVAQTGLIGNLPTH-----KEVFTSESTNYQLAPGEDKLDVRLTWKGDNGVEVHK 175

Query: 164 TFVLKRGDYAVNVNYNVQNAGEKPLEISSFGQLKQSITLPPHLDTGSSNFALHTFRGAAY 223
 + +R YA+ V+Y ++N + ++ S + Q+ + ++ + TF G AY

Sbjct: 176 IYTFRRDSYAEVSYEIRNNSDTAVDPSVYQIVHDN-----QSHQGSYMMPTFTGGAY 229

Query: 224 STPDEKYEKYKFDTIADNENLNISSEKGGWVAMLQQYFATAWIPHNDGTNNFYTANLGNGI 283
 T +KY+K F +A NL+ ++ GWV ++Q YF +AWIP + FYT L + +

Sbjct: 230 YTEADKYKKLSFSDMAKT-NLSKNASDGWGLVQHYFVSAWIPEDGLVREFYTKKLSDNV 288

Query: 284 AAIGYKSQLPVLVQPGQTGAMNSTLWVGPEIQDKMAAVAPHLDTVDYGWLWFISQPLFKL 343
 +IG S + PGQ+ + S L+ GP+ Q ++ +VAP L+ TVDYGWL I+ PLF +

Sbjct: 289 YSIGSVSPLGNIAPGQSVTLKSRLYAGPQTQSELKSVAPGLEYTVDYGWLTVIATPLFWI 348

Query: 344 LKWIHSFVGNWGFSSIIITFIVRGIMYPLTKAQYTSMAKMRMLQPKIQAMRERLGDDKQR 403
 L I V NWG +II++T +++ + YPL+ A Y SMA MR L P++Q ++E+ GDD+Q+

Sbjct: 349 LSSIQKVHNWGVAILLLTILIKLVFYPLSAASYRSMANMRELAPRLQRLKEQYGDQRK 408

Query: 404 ISQEMMALYKAKEKNPLGGCFPLLIQMPIFLALYMLMGSVELRQAPFALWIHDLQAQDP 463
 + Q MM +YK EK+NP+GGC P+L+Q+P+F+ALY++L+GSVE+R APF LWI DLQA DP

Sbjct: 409 LHQAMMEMYKTEKINPMGGCLPILVQIPVFIALYWVLLGSVEMRHAPFMLWIQDLQSAVDP 468

Query: 464 YYILPILMGVTMFFIQKMSPTTVDTPMQQKIMTFMPVIFTVFFLWFPGLVLYYIVSNLV 523
 YY+LPILMG+TM K++P DP+Q K+MT MP++F+VFF +FP+GLVLY++V+N++

Sbjct: 469 YYVLPILMGITMIIQTKLNPKP-ADPIQAKVMTIMPVIVSVFFFFFPAGLVLYWLVNNIL 527

Query: 524 TIIQQQLIYRGLEK 537
 +I QQ I R E+

Sbjct: 528 SIAQQWYINRSTER 541

>ref|ZP_00318461.1| COG0706: Preprotein translocase subunit YidC [Microbulbifer
 degradans 2-40]
 Length = 557

Score = 414 bits (1064), Expect = e-114
 Identities = 223/567 (39%), Positives = 332/567 (58%), Gaps = 38/567 (6%)

Query: 1 MDSQRNLLVIALLFVSMIWAQAW----EQDKNPQPAQQTQTTTTAAGSAADQGVPSG 56
 M+ RN L+ A+L ++++++ W E+ + P Q TT +D V +S

Sbjct: 1 MNWLRNSLIAAILVITYVLFIRWNEFSERQQVPTIANQPAAVTPPAYEAVPSDDAVASSA 60

Query: 57 -----QGKLISVKTDVLDLTINTRGGDVEQA-LLPAYPKELN 92
 Q KL++VKTDVL++ I+T GGDV Q LL + +

Sbjct: 61 TEESDVPEVSVAEPVAAPKAVYQPKLVTVKTDVLEVQIDTNGGDVLQVLLKHLADKAD 120

Query: 93 STQPFQLETSPOFIYQAQSGLTGRDGPDPNPANGPRPLYNVEKDAYVLAEGQNELQVPMT 152
 QPF L+ + Y A+SGL G +GPD G R Y+V K Y L +++ V +T

Sbjct: 121 DNQPFVLMTQNSAHTYVARSGLAGNGPDGAKKG-RAKYSVAKTNYSL-NSDDQVVVDLT 178

Query: 153 YTDAAGNTFTKTFVLKRGDYAVNVNYNVQNAGEKPLEISSFGQLKQSITLPPHLDTGSSN 212
 D TK F + Y ++V Y + N + P +GQ+ + + P + G

Sbjct: 179 L-DQENAQITKRFTFTKSSYLIDVEYIITNRADTPWAAKLYGQIIRDGSEPSYGYMG--- 234

Query: 213 FALHTFRGAAYSTPDEKYEKYKFDTIADNENLNISSEKGGWVAMLQQYFATAWIPHNDGTN 272

+ + GAA +TP+ YEK FD + D + KGGWV+++Q YF +AWIP D TN
 Sbjct: 235 --MRPYLGAAITTPENVYKVSFDDMDDGP-FKVEQKGGWVSLIQHYFISAWIPPKDATN 291
 Query: 273 NFYTANLNGIAAIGYKSQPVLVQPGQTGAMNSTLWVGPEIQDKMAAVAPHLDLTVDYGW 332
 ++ + G + + S+ V P G + + + GP+ ++ ++PHLDLT+DY +
 Sbjct: 292 SYELSSKSGNYVLRFISETTTVAPHSVGTVKAGFYAGPKNIRRLEEISPHLDLTIDYSF 351
 Query: 333 LWFISQPLFKLLKWIHSFVGNWGFSSIIITFIVRGIMYPLTKAQYTSMAKMRMLQPKIQA 392
 LWF++PLF L +IH VGNWG +II++T +++ + + Y SMAKMR LQP +
 Sbjct: 352 LWFIAKPLFFALDFIHGLVGNWGVAILLTVLIKAVFFYPSSAMSYRSMKMRKLQPMMAE 411
 Query: 393 MRERLGDDKQORISQEMMALYKAEKVNPLGGCFPLLIQMPIFLALYYMLMGVELRQAPFA 452
 ++ER G+DKQ++S E+M LYK EKVNP GGC P+L+QMP+F++LY+M+M SVELR PF
 Sbjct: 412 LKERYGEDKQKMSGELMKLYKKEKVNPFGGCLPILLQMPVFISLYWMIMESVELRHQPF 471
 Query: 453 LWIHDLSAQDPYYILPILMGVTMFFIQKMSPTTVDPMQKIMTFMPVIFTVFFLWFPSG 512
 LWI DLS +DP +ILP+LMGVTM+ QK++PT DPMQ K+M MP+ FT F++FP+G
 Sbjct: 472 LWIQDLSVKDPLFILPLMGVTMYIQKLNPTP-PDPMQAKVMQMMPIGFTFLFMFFPAG 530
 Query: 513 LVLYYIVSNLVTIIQQQLIYRGLEKRG 539
 LVLY++V+N ++I QQ +I R +EK G
 Sbjct: 531 LVLYWVNNNTLSISQQYVITRNIKAG 557

>ref|ZP_00152752.2| COG0706: Preprotein translocase subunit YidC [Dechloromonas
 aromatica RCB]
 Length = 547

Score = 406 bits (1043), Expect = e-112
 Identities = 216/559 (38%), Positives = 332/559 (59%), Gaps = 26/559 (4%)

Query: 1 MDSQRNLLVIALLFVSFMIWQAWEQDKNPQPQAQQTQTTTTAA--SAADQGVPSAGQ- 57
 MD++R +LV+ F SFM+W+ W++ P+P + AA SAA Q A G
 Sbjct: 1 MDTRRLILVLIFTFSSFMLWENWQKYNQPKPADAVAAAPVSGAAPTSAALQAKAAPGTP 60
 Query: 58 -----GKLISVKTDVLDLTINTRGGDVEQALLPAYPKELNSTQPFQLLETSPQFIYQ 109
 + S+ TD+L TI+ +GGD+ L Y + + + F L + Q++
 Sbjct: 61 PVATPVSTAETFSITTDLLKATISAQGGDLVSLELLNYKEHDDIQKNFDLFDKHAQYL-- 118
 Query: 110 AQSGLTGRDGPDPNPANGPRPLYNVEKDAYVLAEGQNELQVPMTYTDAAGNTFTKTFVLKR 169
 AQ+GL G P + R + A LA+G +EL+V + D G K KR
 Sbjct: 119 AQAGLIGELPTH-----RTTFKHVGGATKLADGTDELKVRLESADQNGIKVAKILTFKR 173
 Query: 170 GDYAVNVNYNVQNAGEKPLEISSFGQLKQSITLPPHLDTGSSNFALHTFRGAAYSTPDEK 229
 G Y +++ + V N +K + ++ QL++ P + TF G A T +K
 Sbjct: 174 GSYLIDIAWEVANGSDKAIAPHAYYQLQRDDLAP-----AGETKMVSTFTGPAVFTDADK 228
 Query: 230 YEKYKFDTIADNE-NLNISSKGGWVAMLQQYFATAWIPHNDGTNNFYTANL-GNGIAAIG 287
 Y+K F+ IADN+ ++ GW+AM+Q YF +AW+P + FY + G+ + G
 Sbjct: 229 YQKVTFEHIADNKAKFTKTADNGWLAMVQHYFVSAWVPKDKTQREFYMRKVEGSNVFQAG 288
 Query: 288 YKSQPVLVQPGQTGAMNSTLWVGPEIQDKMAAVAPHLDLTVDYGWLWLFISQPLFKLLKWI 347
 + PG G + +L+ GP++Q + VAP LDL VDYGWL ++ P+F L+ I
 Sbjct: 289 VIVPVAEIAPGAKGEASVSLYAGPQMQSALKQVAPGLDLVVDYGWLTVVAAPIFWALEAI 348
 Query: 348 HSFVGNWGFSSIIITFIVRGIMYPLTKAQYTSMAKMRMLQPKIQAMRERLGDDKQORISQE 407
 H VGNWG++I+++T +++ + +PL+ A Y SMAKM+ML P++ ++ER GDDKQOR++QE
 Sbjct: 349 HKLVGNWGWAIIVLTIMIKAVFFPLSAASYKSMAKMKMLTPRLAQLKERFGDDKQRLNQE 408

Query: 408 MMALYKAEKVNPLGGCFPLLIQMPIFLALYYMLMGSVELRQAPFALWIHDLAQDPYYIL 467
 MM LY+ EKVNPLGGC P+L+Q+P+F+ALY++L+G+VE+R AP+ LWI DL++ DPYYIL
 Sbjct: 409 MMKLYQTEKVNPLGGCLPILVQIPVFIALYWVLLGAVEMRGAPWILWIKDLASADPYYIL 468

Query: 468 PILMGVTMFFIQKMSPTTVDTPMQQKIMTFMPVIFTVFFLWFPGLVLYYIVSNLVTIIQ 527
 P++M V+MF K++PT DP+Q K+M MP+IF F WFP+GLVLY++V+N+++I Q
 Sbjct: 469 PVIMMVSMEVQTKLNPTP-PDPIQAKVMMMPLI FGFMFFWFPAGLVLYWVNNVLSIAQ 527

Query: 528 QQLIYRGLEKRLHSREKK 546
 Q I R ++ G + + K
 Sbjct: 528 QWQITRLIDAGGKAANDAK 546

>ref|NP_879348.1| probable inner-membrane protein [Bordetella pertussis Tohama I]
 Length = 563

Score = 385 bits (990), Expect = e-106
 Identities = 212/575 (36%), Positives = 328/575 (57%), Gaps = 56/575 (9%)

Query: 1 MDSQRNLLVIALLFVSFMIWQAWEQDKN-----PQPQAQQTQTQTTTTAAGSAADQ--- 50
 MD +R +L + F ++W W+ P P+A T Q A G+AA
 Sbjct: 1 MDIRRTVLWMIFSFSLLLLWNNWQIHNGKPSLFGGPAPEAAATQPKADANGTAASSTAS 60

Query: 51 -----GVPASGQGKLISVKTDVLDLTINTRGGDVEQALLPAYPKELNS 93
 PA+ + + + TDVL LT ++ G + +A L YP S
 Sbjct: 61 IPSSPAAAPAAASVPGAAAPAAKSEQVITTDVLRLTDFSNGAQLIRAELLKYPSSSSQS 120

Query: 94 TQPFQLLETSPQFIYQAQSGLTGRDGPDPNANGPRPLYNVEKDAYVLAEGQNELQVPMY 153
 +P L++ S +Y AQ+G+ G ++ P + V + + + L V
 Sbjct: 121 DKPTVLMDRSADLVYVAQTGVVGAPQGESFPTHQTPFHLVSSERSLTGD---TLDVVFE- 176

Query: 154 TDAAGNTFTKTFVLKRGDYAVNVNYNVQNAGEKPLEISSFGQLKQSITLPPHLDTGSSNF 213
 ++ G TKT+ L RG Y V+V + + N G PL + + QL++ T P G+S+F
 Sbjct: 177 AESGGLKVTKYTLHRGRYDQVDRHAMANTGGAPLNALYLQLERDGTDP----AGTSSF 232

Query: 214 ALHTFRGAAYSTPDEKYEKYKFDTIADNENLNIS-SKGGWVAMLQQYFATAWIPHN--DG 270
 HTF G A + +K++K F I + I + GW+ ++Q YFATAWIP
 Sbjct: 233 -YHTFTGVAVYSEQDKFQKVTFSIDIEKKKGTIYKQADNGWIGIVQHYFATAWIPAQGKQR 291

Query: 271 TN-----NFYTANLNGIAAIGYKSQPVLVQPGQTGAMNSTLWVGPEIQDKMAAVAPH 323
 TN N Y A I A+G + PG + +++ LWVGP+ Q MAAVAP
 Sbjct: 292 TNELQVQQLNYAART---IEAVG-----TIAPGSSANVDAHLWVGPDQKAMAAPAG 342

Query: 324 LDLTVDYDGLWLFISQPLFKLLKWIHSFVGNWGFSSIIITFIVRGIMYPLTKAQYTSMAKM 383
 L+L VDYDGL I++PLF L+ W+H +GNWG++I+ +T I++ + +PL A Y SMA+M
 Sbjct: 343 LELVDYDGLTIIAKPLFTLMTWLHGLLGNWGTIVALTVIIKAVFFPLAAASYRSMARM 402

Query: 384 RMLQPKIQAMRERLGDDKQRISEMMALYKAEKVNPLGGCFPLLIQMPIFLALYYMLMGS 443
 + + P++QA++E+ GDD+Q+++Q MM +Y+ EK+NPLGGC P+++Q+P+F+ALY++L+ S
 Sbjct: 403 KQVAPRLQALKEKYGDDRQKLNQAMMEMYRTEKINPLGGCLPMVVQIPVFIALYWVLLAS 462

Query: 444 VELRQAPFALWIHDLAQDPYYILPILMGVTMFFIQKMSPTTVDTPMQQKIMTFMPVIFT 503
 VE+R AP+ LW+HDL +DP++ILP +M TMF K++PT DP+Q K+M MP++F
 Sbjct: 463 VEMRGAPWILWVHDLSDVRDPFFILPAIMMATMFLQIKLNPTP-PDPVQAKVMMIMPLVFG 521

Query: 504 VFFLWFPGLVLYYIVSNLVTIIQQQLIYRGLEKR 538
 +FP+GLVLY+ V+N ++I QQ I R LE++
 Sbjct: 522 GMMFFFFPAGLVLYWCVNNTLSIAQQWTITRNLERQ 556

>ref|ZP_00334719.1| COG0706: Preprotein translocase subunit YidC [Thiobacillus
denitrificans ATCC 25259]
Length = 546

Score = 384 bits (987), Expect = e-106

Identities = 214/553 (38%), Positives = 315/553 (56%), Gaps = 28/553 (5%)

Query: 1 MDSQRNLLVIALLFVSFMIWQAWQDKNPQPQAQQTQTTTTAAGSAADQ-----GVPAS 55
MD+QR +L I F ++W+AW+ + P P T AGSAA PA+
Sbjct: 1 MDNQRLLILFIVFSFSLLLLWEAWQDKQAPAPA---TRPVAGAPAGSAAPTSTALNAPAA 57

Query: 56 G-----QGKLISVKTDVLDLTINTRGGDVEQALLPAYPKELNSTQPFQLLETSPQFIY 108
+G V+TDVL TI+ GGD+ + L Y + + + F L E S Y
Sbjct: 58 APAQTGFAKGARAVVETDVLRTIDANGGDLRELQLLGYRETEDKNRVFTLTFEDSRTRPY 117

Query: 109 QAQSGLTGRDGPDPNPANGPRPLYNVEKDAYVLAEGQNELQVPMTYTDAA-GNTFTKTFVL 167
AQSG G P + R + + Y L G L+VP+ + DAA G KTF+
Sbjct: 118 LAQSGFVGGGLPTH-----RSTFELTPGTYRLTGGAARLEVPLVWDAARGVRVEKTFIF 172

Query: 168 KRGDYAVNVNYNVQNAGEKPLEISSFGQLKQSITLPPHLDTGSSNFALHTFRGAAYSTPD 227
RG + V V V N G++PL+++ + Q + P +F L+T+ G A+ T
Sbjct: 173 TRGSHEVAVRTRVNRGKEPLDLTPYYQFTRHGEAPR-----GESFFLYTYTGPAFYTDA 227

Query: 228 EKYEKYKFDTIADNE-NLNISSKGGWVAMLQQYFATAWIPHNDGTNNFYTANLGNGIAAI 286
+K++K F I D ++ GWV ++Q +F AW+P +Y +LG G+ +
Sbjct: 228 KKFQKVPFTDIQDGSAEFEKTATNGWVGLVQHFFVAAWLPEESVKREYYARSLGEGLYSA 287

Query: 287 GYKSQPVLVQPGQTGAMNSTLWVGPEIQDKMAAVAPHLDLTVDYGWLWFISQPLFKLLKW 346
G + PGQ L+ GP+ Q + AP LDL DYGWL ++ P+F L+
Sbjct: 288 GVILAEGQLAPGQKQKTFVTPLYAGPQSQAVLEKAAPGLDLARDYGWLTPLAYPIFWSLEK 347

Query: 347 IHSFVGNWGFSSIIITFIVRGIMYPLTKAQYTSMAKMRMLQPKIQAMRERLGDDKQORISQ 406
I VGNWG++IIII+T +++ +YPL+ A Y SMAKM+ L P++Q ++E GDD+ ++ Q
Sbjct: 348 IERLVGNWGWAIILITILIKLALYPLSAAGYKSMAMKKLTPRLQQLKETYGDDRAKLHQ 407

Query: 407 EMMALYKAEKVNPLGGCFPLLIQMPIFLALYYMLMGSVELRQAPFALWIHDLQAQDPYYI 466
M +YK EK+NPLGGC P+LIQ+P+F+ALY++L+ +VE+R AP+ WI DL+A DP+YI
Sbjct: 408 AMAEMYKTEKINPLGGCLPILIQIPVFIALYWVLLAAVEMRGAPWLGWITDLTAPDPWYI 467

Query: 467 LPILMGVTMFFIQKMSPTTVTDPMQKIMTFMPVIFTVFFLWFPGLVLYYIVSNLVTII 526
LPI+MGVT K++P + DPMQ KIM MPV FTV F++FP+GLVLY++V+N+++I
Sbjct: 468 LPIIMGVTSILQVKLNQPM-DPMQAKIMMIMPVAFVTFVFFPAGLVLYWVNNILSIA 526

Query: 527 QQQLIYRGLEKRG 539
QQ I + +E G
Sbjct: 527 QQWAINKQVEGSG 539

>ref|NP_891527.1| probable inner-membrane protein [Bordetella bronchiseptica RB50]
Length = 554

Score = 380 bits (975), Expect = e-104

Identities = 208/562 (37%), Positives = 321/562 (57%), Gaps = 56/562 (9%)

Query: 14 FVSEMIWQAWQDKN-----PQPQAQQTQTTTTAAGSAADQ----- 50
F ++W W+ P P+A T Q A G+AA
Sbjct: 5 FSLLLLWNNWQIHNGKPSLFGGPAPEAAATQOPKADANGTAASSTASIPSSPAAAPAAAS 64

Query: 51 ----GVPASGQGKLISVKTDVLDLTINTRGGDVEQALLPAYPKELNSTQPFQLLETSPQF 106
 PA+ + + + + TDVL LT ++ G + +A L YP S +P L++ S
 Sbjct: 65 VPGAAAPAAAKSEQVVITTDVLRLLTFDSNGAQLIRAEALLKYPSSSSQSDKPTVLMDRSADL 124

Query: 107 IYQAQSGLTGRDGPDPNPANGPRPLYNVEKDAYVLAEGQNELQVPMTYTDAAGNTFTKTFV 166
 +Y AQ+G+ G ++ P + V + + + L V ++ G TKT+
 Sbjct: 125 VYVAQTGVVGAPQGESFPTHQTPFHLVSSERSLTGD---TLDVVFE-AESGGLKVTKTYT 180

Query: 167 LKRGDYAVNVNINVQNAGEKPLEISSFGQLKQSITLPPHLDTGSSNFALHTFRGAAYSTP 226
 L RG Y V+V + + N G PL + + QL++ T P G+S+F HTF G A +
 Sbjct: 181 LHRGRYDVRHAMANTGGAPLNPALYLQLERDGTDP----AGTSSF-YHTFTGVAVYSE 235

Query: 227 DEKYEKYKFDTIADNENLNIS-SKGGWVAMLQQYFATAWIPHN--DGTN-----NFYT 276
 +K++K F I + I + GW+ ++Q YFATAWIP TN N Y
 Sbjct: 236 QDKFQKVTFSDIEKKKGTIYKQADNGWIGIVQHYFATAWIPAQKQRTNELLQVQQNLYA 295

Query: 277 ANLGNIAAIGYKSQPVLVQPGQTGAMNSTLWVGPEIQDKMAAVAPHLDLTVDYGWLWFI 336
 A I A+G + PG + +++ LWVGP+ Q MAAVAP L+L VDYGWL I
 Sbjct: 296 ART---IEAVG-----TIAPGSSANVDAHLWVGPDQKAMAAPGLELVVDYGWLTI 346

Query: 337 SQPLFKLLKWIHSFVGNWGFSSIIITFIVRGIMYPLTKAQYTSMAKMRMLQPKIQAMRER 396
 ++PLF L+ W+H +GNWG++I+ +T I++ + +PL A Y SMA+M+ + P++QA++E+
 Sbjct: 347 AKPLFTLMTWLHGLLGNWGTIVALTVIIKAVFFPLAAASYRSMARMKQVAPRLQALKEK 406

Query: 397 LGDDKQRISQEMMALYKAEKVNPLGGCFPLLIQMPIFLALYYMLMGSVELRQAPFALWIH 456
 GDD+Q+++Q MM +Y+ EK+NPLGGC P+++Q+P+F+ALY++L+ SVE+R AP+ LW+H
 Sbjct: 407 YGDDRQKLNQAMMEMYRTEKINPLGGCLPMVQIPVFIALYWVLLASVEMRGAPWILWVH 466

Query: 457 DLSAQDPYIILPILMGVTMFFIQKMSPTTVTDPMQKIMTFMPVIFTVFFLWFPSGLVLY 516
 DLS +DP++ILP +M TMF K++PT DP+Q K+M MP++F +FP+GLVLY
 Sbjct: 467 DLSVRDPFFILPAIMMATMFLQIKLNPTP-PDPVQAKVMMIMPLVFGGMMFFFPAGLVLY 525

Query: 517 YIVSNLVTIIQQQLIYRGLEKR 538
 + V+N ++I QQ I R LE++
 Sbjct: 526 WCVNNTLSIAQQWTITRNLERQ 547

>ref|NP_886531.1| probable inner-membrane protein [Bordetella parapertussis 12822]
 Length = 554

Score = 380 bits (975), Expect = e-104

Identities = 208/562 (37%), Positives = 321/562 (57%), Gaps = 56/562 (9%)

Query: 14 FVSFMIWQAWSEQDKN-----PQPQAQQTQTTTTAAAGSAADQ----- 50
 F ++W W+ P P+A T Q A G+AA
 Sbjct: 5 FSLLLLWNNWQIHNGKPSLFGGPAPEAAATQPKADANGTAASSTASIPSSPAAAPAAAS 64

Query: 51 ----GVPASGQGKLISVKTDVLDLTINTRGGDVEQALLPAYPKELNSTQPFQLLETSPQF 106
 PA+ + + + + TDVL LT ++ G + +A L YP S +P L++ S
 Sbjct: 65 VPGAAAPAAAKSEQVVITTDVLRLLTFDSNGAQLIRAEALLKYPSSSSQSDKPTVLMDRSADL 124

Query: 107 IYQAQSGLTGRDGPDPNPANGPRPLYNVEKDAYVLAEGQNELQVPMTYTDAAGNTFTKTFV 166
 +Y AQ+G+ G ++ P + V + + + L V ++ G TKT+
 Sbjct: 125 VYVAQTGVVGAPQGESFPTHQTPFHLVSSERSLTGD---TLDVVFE-AESGGLKVTKTYT 180

Query: 167 LKRGDYAVNVNINVQNAGEKPLEISSFGQLKQSITLPPHLDTGSSNFALHTFRGAAYSTP 226
 L RG Y V+V + + N G PL + + QL++ T P G+S+F HTF G A +
 Sbjct: 181 LHRGRYDVRHAMANTGGAPLSPALYLQLERDGTDP----AGTSSF-YHTFTGVAVYSE 235

Query: 227 DEKYEKYKFDTIADNENLNIS-SKGGWVAMLQQYFATAWIPHN--DGTN-----NFYT 276
 +K++K F I + I + GW+ ++Q YFATAWIP TN N Y
 Sbjct: 236 QDKFQKVTFSDIEKKKGTYIKQADNGWIGIVQHYFATAWIPAQGKQRTNELLOVQOONLYA 295

Query: 277 ANLGNGIAAIGYKSQPVLVQPGQTGAMNSTLWVGPEIQDKMAAVAPHLDLTVDYGWLWFI 336
 A I A+G + PG + +++ LWVGP+ Q MAAVAP L+L VDYGWL I
 Sbjct: 296 ART---IEAVG-----TIAPGSSANVDAHLWVGPDQKAMAAPGLELVVDYGWLTII 346

Query: 337 SQPLFKLLKWIHSFVGNWGFSSIIITFIVRGIMYPLTKAQYTSMAKMRMLQPKIQAMRER 396
 ++PLF L+ W+H +GNWG++I+ +T I++ + +PL A Y SMA+M+ + P++QA++E+
 Sbjct: 347 AKPLFTLMTWLHGLLGNWGTIVALTVIIKAVFFPLAAASYRSMARMKVAPRLQALKEK 406

Query: 397 LGDDKQRISQEMMALYKAEKVNPLGGCFPLLIQMPIFLALYYMLMGSVELRQAPFALWIH 456
 GDD+Q+++Q MM +Y+ EK+NPLGGC P+++Q+P+F+ALY++L+ SVE+R AP+ LW+H
 Sbjct: 407 YGDDRQKLNQAMMEMYRTEKINPLGGCLPMVVQIPVFIALYWVLLASVEMRGAPWILWVH 466

Query: 457 DLSAQDPYYILPILMGVTMFFIQKMSPTTVDPMQQKIMTFMPVIFTVFFLWFPSGLVLY 516
 DLS +DP++ILP +M TMF K++PT DP+Q K+M MP++F +FP+GLVLY
 Sbjct: 467 DLSVRDPFFILPAIMMATMFLQIKLNPTP-PDPVQAKVMMIMPLVFGGMMFFFPAGLVLY 525

Query: 517 YIVSNLVTIIQQQLIYRGLEKR 538
 + V+N ++I QQ I R LE++
 Sbjct: 526 WCVNNTLSIAQQWTITRNLERQ 547

>ref|NP_840474.1| 60Kd inner membrane protein [Nitrosomonas europaea ATCC 19718]
 Length = 614

Score = 379 bits (974), Expect = e-104

Identities = 206/564 (36%), Positives = 322/564 (57%), Gaps = 47/564 (8%)

Query: 1 MDSQRNLLVIALLFVSFMIWQAW--EQDKNPQP----QAQQTQT----- 40
 MD+++ +L+I +W AW EQ+K P QA + +T
 Sbjct: 1 MDNKKIVLLIIFSTSLFLWDAWIKEQEKFNNPPAITQADSSAGSTQSRNDDSLPVPGE 60

Query: 41 -TTAAGSAADQGV PASG-----QGKLISVKTDVLDLTINTRGGDVEQALLPAY 87
 T++ S G+PASG G+ I V TD + I+T GGD+ + L
 Sbjct: 61 LTSSQASPDNTGIPASGGNGDSVTPRLLPSGEQIRVVTDKIVIAEIDTIGGDLRRLLELLQ 120

Query: 88 PKELNSTQPFQLETSPQFIYQAQSGLTGRDGPDPNANGPRPLYNVEKDA--YVLAEGQN 145
 P + P+ LL + Y AQSG L G P++ + + E D Y L+ G++
 Sbjct: 121 PSSEDKDTPYALLYSEAARTYIAQSGLVGEGLPNH-----KTTFRAESDIRNYELSSGED 175

Query: 146 ELQVPMTYTDAAGNTFTKTFVLKRGDYAVNVNYNVQNAGEKPLEISSFGQLKQSITLPPH 205
 ++ + + +A G KT+ R Y ++V + V+N G+ + ++ Q+ + PP
 Sbjct: 176 KIVIRLLAPEAQGVQVIKTYTFHRDSYVIDVGFEVENKGDATVRPFAYFQMLRDGNPPP- 234

Query: 206 LDTGSSNFALHTFRGAAYSTPDEKYEKYKFDTIADNE-NLNIS SKGGWVAMLQQYFATAW 264
 + + TF GAA T + KY+K F + N+ + ++ GW+AML+ YF TAW
 Sbjct: 235 ----AKTMMIPTFLGAAYVTEEGKYQKIPFSDLDKNKADYPANANNGWIAMLEHYFLTAW 290

Query: 265 IPHNDGTNNFYTANLGNGIAAIGYKSQPVLVQPGQTGAMNSTLWVGPEIQDKMAAVAPHL 324
 +P F+ + + + G ++ PG+ A + GPE QD + +AP L
 Sbjct: 291 LPQQQTPREFFAKRQSDNLYSAGVIVPAGVIAPGEIAATTMPFYAGPEEQDNLEGLAPGL 350

Query: 325 DLTVDYGWLWFI SQPLFKLLKWIHSFVGNWGFSSIIITFIVRGIMYPLTKAQYTSMAKMR 384
 DLTVDYGWL I++PLF+LL + HS+ NWG +II++T V+ + +PL+ A Y SMAK+R
 Sbjct: 351 DLTVDYGWLTVIAKPLFRLLSFYHSWTDNNGVAIILLTMTVKLLFFPLSAAGYRSMALR 410

Query: 385 MLQPKIQAMRERLGDDKQRISEQEMMALYKAEKVNPLGGCFPLLIQMPIFLALYYMLMGSV 444
 ++ PK++ +++++ D+QR+ Q MM YK EK+NP+GGCFP+L+Q+P+F+ALY+ ++ +V
 Sbjct: 411 LVTPKPKRIQDQYKGRQRMHQAMMEFYKEEKINPMGGCFPILVQIPVFIALYWTILAAV 470

Query: 445 ELRQAPFALWIHDLAQDPYYILPILMGVTMFFIQKMSPTTVTDPMQQKIMTFMPVIFTV 504
 ELR AP ALWI DLS+ DP+Y+LP+IMG++MF K++PT TDP+Q KIM MPV F+
 Sbjct: 471 ELRYAPLALWIDDLSSDPFYMLPLLMGISMFEVQTKLNPTP-TDPLQAKIMQIMPVAFSA 529

Query: 505 FFLWFPSGLVLYYIVSNLVTIIQQ 528
 F +FP+GLVLY +V+N+++I QQ
 Sbjct: 530 IFFFFPAGLVLYSLVNNILSIAQQ 553

>ref|ZP_00277425.1| COG0706: Preprotein translocase subunit YidC [Burkholderia fungo
 LB400]
 Length = 552

Score = 375 bits (962), Expect = e-103
 Identities = 210/559 (37%), Positives = 317/559 (56%), Gaps = 43/559 (7%)

Query: 1 MDSQRNLLVIALLFVSFMIWQAWEQDKNPQ-----PQAQQTQTTTTAAGS----- 46
 MD +R +L + + M++ W++D P A T + A G+
 Sbjct: 1 MDIKRTVLWVIFMSAVMLFDNWQRDHGRPSMFFPSATPTRTVGSAAPGTTTTPGTQPADL 60

Query: 47 -----AADQGV PASGQGLISVKTDVLDLTINTRGGDVEQALLPAYPKELNSTQP---FQ 98
 AA PA+ Q +LI TDV I+TRGG + + L K+ + QP
 Sbjct: 61 PATNAAAPGNAPAAATQSQLIKFNTDVYSGEIDTRGGTSLKSLV---KQGDGKQPDLVIT 117

Query: 99 LLETSPQFIYQAQSGLTGRDGPDPNPANGPRPLYNVEKDAYVLAEGQNELQVPMTYTDAAG 158
 L + + Y A++GL G D P N + PL N D L + Q+ G
 Sbjct: 118 LFDRTANHTYLARTGLLGDFP-NHNDIYTPLNQPHD---LTGDEKSFQISFESPVKGG 173

Query: 159 NTFTKTFVLKRGDYAVNVNYNVQNAGEKPLEISSFGQL---KQSITLPPHLDTGSSNFAL 215
 KT+ RG Y + V+ +QN G P+ S + +L Q + P F+
 Sbjct: 174 VKVIKTYTFTGRGSYVIGVDTKIQNVGTTVPVSPSVYMELVRDDQPVETP-----RFS- 224

Query: 216 HTFRGAAYSTPDEKYEKYKFDTIADN-ENLNISCKGGWVAMLQQYFATAWIPHNDGTNNF 274
 HTF G A T ++K F I N ++ S+ GW+AM+Q YFA+AWIP +
 Sbjct: 225 HTFIGPAVYTDQHHFQKMTFGDIDKNKQDYATSADNGWIAMVQHYFASAWIPQQGAKRDI 284

Query: 275 YTANLNGIAAIGYKSQPVLVQPGQTGAMNSTLWVGPEIQDKMAAVAPHLDLTVDYGWLW 334
 Y + + +G K + PGQT +++ L+ GPE + + +AP L+L DYGW+
 Sbjct: 285 YVEKIDPALYRVGVKEPVPTIAPGQTVDV SARLFAGPEEERMLEGIAPGLELVKDYGWVT 344

Query: 335 FISQPLFKLLKWIHSFVGNWGFSSIIITFIVRGIMYPLTKAQYTSMAKMRMLQPKIQAMR 394
 I++PLF LL+ IHS+VGNWG+SI+++T +++ + +PL+ A Y SMA+M+ + P++QA+R
 Sbjct: 345 IIAKPLFWLLEKIHSYVGNWGSIVLLTLLIKAVFFPLSAASYKSMARMKAITPRMQALR 404

Query: 395 ERLGDDKQRISEQEMMALYKAEKVNPLGGCFPLLIQMPIFLALYYMLMGSVELRQAPFALW 454
 ER D Q+++ +M LYK EKVNP GGC P++IQ+P+F++LY++L+ SVE+R AP+ LW
 Sbjct: 405 ERFKGDPPQKMNSALMELYKTEKVNPFGGCLPVVIQIPVFISLYWVLLSSVEMRGAPWILW 464

Query: 455 IHDLSAQDPYYILPILMGVTMFFIQKMSPTTVTDPMQQKIMTFMPVIFTVFFLWFPSGLV 514
 IHDLS QDP++ILP+LM V+MF K++PT DP+Q K+M FMP+ F+V F +FP+GLV
 Sbjct: 465 IHDLSQQDPFFILPVLMAVSMFLQTKLNPTP-PDPVQAKMMFMPIAFSVMFFFFPAGLV 523

Query: 515 LYYIVSNLVTIIQQQLIYR 533
 LYY+V+N+++I QQ I R

Sbjct: 524 LYYVVNNVLSIAQQYYITR 542

>ref|YP_106704.1| putative membrane protein [Burkholderia pseudomallei K96243]
Length = 558

Score = 369 bits (948), Expect = e-101

Identities = 202/562 (35%), Positives = 316/562 (56%), Gaps = 41/562 (7%)

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Query: 1  MDSQRNLLVIALLFVSFMIWQAWEQDKN-PQPQAQQTQTQTTT-----AAGSAA 48
          MD +R +L +      + M++ W++ P      TQT T      A+ +AA
Sbjct: 1  MDIKRTVLWVIFFMASVMLFDNWQRSHGRPSMFFPNVTQNTASNATNGNGASGASAAAA 60

Query: 49  DQGVSPASGQG-----KLISVKTDVLDLTINTRGGDVEQALLPAYPKELNSTQP 96
          +PA+ G      +L+ TDV + I+TRGG + + L
Sbjct: 61  ANALPAAATGAAPATTAPAAQAQLVRFSTDVYNGEIDTRGGTLAKLTLTKAGDGKQPDLS 120

Query: 97  FQLETSPPQFIYQAQSGLTGRDGPDPNPANGPRPLYNVEKDAYVLAEGQNELQVPMTYTDA 156
          L + + Y A++GL G D P++ +Y      LA QN L++
Sbjct: 121 VTLFDHTANHTYLARTGLLGDFPNH-----NDVYAQVAGPTSLAADQNTLKLSEFSPVK 175

Query: 157  AGNTFTKTFVLKRGDYAVNVNYNVQNAGEKPLEISSFGQLKQSITLPPHLDTGSSNFAL- 215
          G KT+ RG Y + V+ ++N G P+ S + +L +      D S +
Sbjct: 176 GGKVKVKTFTFTRGSYVIGVDTKIENVGAAPVTPSVYMELVR-----DNSSVETPMF 227

Query: 216  -HTFRGAAYSTPDEKEYEKYKFDTIADNE-NLNISSKGGWVAMLQQYFATAWIPHNDGTNN 273
          HTF G A T + ++K F I N+ + S+ GW+AM+Q YFA+AWIP + +
Sbjct: 228 SHTFLGPAVYTDQKHFKITFGDIDKNKADYVTSADNGWIAMVQHYFASAWIPQSGAKRD 287

Query: 274  FYTANLGNIAAIGYKSQPVLVQPGQTGAMNSTLWVGPEIQDKMAAVAPHLDLTVDYGWL 333
          Y + + +G K + PGQ+ +++ L+ GPE + + +AP L+L DYGW+
Sbjct: 288 IYVEKIDPTLYRVGVKQPVAAIAPQSADVSARLFAGPEEERMLEGIAPGLELVKDYGVW 347

Query: 334  WFISQPLFKLLKWIHSFVGNWGFSSIIITFIVRGIMYPLTKAQYTSMAKMRMLQPKIQAM 393
          I++PLF LL+ IH FVGNWG++I+++T +++ + +PL+ A Y SMA+M+ + P++QA+
Sbjct: 348 TIIAKPLFWLLEKIHFVGNWGWAIVLLTLLIKAVFFPLSAASYKSMARMKEITPRMQAL 407

Query: 394  RERLGDDKQRISQEMMALYKAKEKNPLGGCFPLLIQMPIFLALYYMLMGSVELRQAPFAL 453
          RER D Q+++ +M LYK EKNP GGC P++IQ+P+F++LY++L+ SVE+R AP+ L
Sbjct: 408 RERFKSDPQKMNAALMELYKTEKVNPFPGCLPVVIQIPVFISLYWVLLASVEMRGAPWVL 467

Query: 454  WIHDLAQDPYYILPILMGVTMFFIQKMSPTTVDTPMQQKIMTFMPVIFTVFLLWFPSGL 513
          WIHDL +DPY+ILP+LM V+MF K++PT DP+Q K+M FMP+ F+V F +FP+GL
Sbjct: 468 WIHDLQRDPYFILPVLMAVSMFVQTKLNPTP-PDPVQAKMMFMPIAFSVMFFFFFPAGL 526

Query: 514  VLYYIVSNLVTIIQQQLIYRGL 535
          VLYY+V+N+++I QQ I R L
Sbjct: 527 VLYYVVNNVLSIAQQYYITRTL 548

```

>ref|YP_104854.1| inner membrane protein, 60 kDa [Burkholderia mallei ATCC 23344]
Length = 558

Score = 369 bits (946), Expect = e-101

Identities = 202/562 (35%), Positives = 316/562 (56%), Gaps = 41/562 (7%)

```

Query: 1  MDSQRNLLVIALLFVSFMIWQAWEQDKN-PQPQAQQTQTQTTT-----AAGSAA 48
          MD +R +L +      + M++ W++ P      TQT T      A+ +AA

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Sbjct: 1 MDIKRTVLWVIFMSAVMLFDNWQRSHGRPSMFFPNVTQNTASNATNGNGASGASAAAA 60

Query: 49 DQGV PASGQG-----KLISVKTDVLDLTINTRGGDVEQALLPAYPKELNSTQP 96
+PA+ G +L+ TDV + I+TRGG + + L

Sbjct: 61 ANALPAAATGAAPATTAPAAQAQLVRFSTDVNGEIDTRGGTLAKLTLTKAGDGKQPDLS 120

Query: 97 FQLETS PQFIYQAQSGLTGRDGPDPNPANGPRPLYNVEKDAYVLAEGQNELQVPMTYTDA 156
L + + Y A++GL G D P++ +Y. LA QN L++

Sbjct: 121 VTFLDHTANHTYLARTGLLGDFPNH-----NDVYAQVAGPTSLAADQNTLKLSEFSPVK 175

Query: 157 AGNTFTKTFVLKRGDYAVNVNYNVQNAGEKPLEISSFGQLKQSITLPPHLDTGSSNFAL- 215
G KT+ RG Y + V+ ++N G P+ S + +L + D S +

Sbjct: 176 GGVKVVKTYTFTTRGSYVIGVDTKIENVGAAPVTPSVYMEVLR-----DNSSVETPMF 227

Query: 216 -HTFRGAAYSTPDEKEYEKYKFDTIADNE-NLNISSKGGWVAMLQQYFATAWIPHNDGTNN 273
HTF G A T + ++K F I N+ + S+ GW+AM+Q YFA+AWIP + +

Sbjct: 228 SHTFLGPAVYTDQKHFKITFGDIDKNKADYVTSADNGWIAMVQHYFASAWIPQSGAKRD 287

Query: 274 FYTANLGNIAAIGYKSQPVLVQPGQTGAMNSTLWVGPEIQDKMAAVAPHLDLTVDYGWL 333
Y + + +G K + PGQ+ +++ L+ GPE + + +AP L+L DYGW+

Sbjct: 288 IYVEKIDPTLYRVGVKQPVETAIAPGQSADVSARLFAGPEEERMLEGIAPGLELVKDYGWV 347

Query: 334 WFISQPLFKLLKWIHSFVGNWGFSSIIITFIVRGIMYPLTKAQYTSMAKMRMLQPKIQAM 393
I++PLF LL+ IH FVGNWG++I+++T +++ + +PL+ A Y SMA+M+ + P++QA+

Sbjct: 348 TIIAKPLFWLLEKIHFVGNWGWAIVLLTLLIKAVFFPLSAASYKSMARMKEITPRMQAL 407

Query: 394 RERLGDDKQRISQEMMALYKAQKVNPLGGCFPLLIQMPIFLALYYMLMGSVELRQAPFAL 453
RER D Q+++ +M LYK EKNP GGC P++IQ+P+F++LY++L+ SVE+R AP+ L

Sbjct: 408 RERFKSDPQKMNAALMELYKTEKVNPFGGCLPVVIQIPVFISLYWVLLASVEMRGAPWVL 467

Query: 454 WIHDLAQDPYIILPILMGVTMFFIQQMSPTTVDTPMQQKIMTFMPVIFTVFVFLWFPSGL 513
WIHDL +DPY+ILP+LM V+MF K++PT DP+Q K+M FMP+ F+V F +FP+GL

Sbjct: 468 WIHDLQSDPYFILPVLMAVSMFVQTKLNPTP-PDPVQAKMMFMPIAFSVMFFFFFPAGL 526

Query: 514 VLYYIVSNLVTIIQQQLIYRGL 535
VLYY+V+N+++I QQ I R L

Sbjct: 527 VLYYVVNNVLSIAQQYYITRTL 548

>ref|ZP_00242356.1| COG0706: Preprotein translocase subunit YidC [Rubrivivax
gelatinosus PM1]
Length = 550

Score = 365 bits (937), Expect = e-100

Identities = 213/556 (38%), Positives = 310/556 (55%), Gaps = 34/556 (6%)

Query: 4 QRNLLVIALLFVSFMIWQAWAQDKN-----PQPQAQQTQTQTTTAAGS---AADQGV 52
+R LL + ++W AW + P+P A + T A S +A

Sbjct: 2 RRTLLWVVFMTSLVLLWDANKHTGQPSMFAPAPRPVAAASAPGVTPPASSVLPSATAVA 61

Query: 53 PASGQ GK-----LISVKTDVLDLTINTRGGDVEQALLPAYPKELNSTQPFQLL 100
PA+G G ++V TDVL LT+++RGGDV A L + + T+ L

Sbjct: 62 PAAGSGAPPALVAPPATAPTVTSTVDVLKLTLDSTRGGDVVHAELLTQVDQNDRTNRNVVLF 121

Query: 101 ETSPQFIYQAQSGLTGRDGPDPNPANGPRPLYNVEKDAYVLAEGQNELQVPMTYTDAAGNT 160
+ S + +Y AQ+GL G PD P + Y + LA G++ L+V + G

Sbjct: 122 DRSKERVYLAQTGLVG--APDLPNH--LTAYTLVPGETSLAAGKDALEVVFESPEQGGVK 177

Query: 161 FTKTFVLKRGDYAVNVNYNVQNAGEKPLEISSFGQLKQSITLPPHLDTGSSNFALHTFRG 220

KT L+RG+YAV V ++V N G L + QL + PP G S+F TF G
 Sbjct: 178 LRKTLTLQRGNVAVQVRHDTVNTGTAALSPQLYVQLVRDGNAPP-----GESSF-YSTFTG 232
 Query: 221 AAYSTPDEKEYEKYKFDTIAD-NENLNISSEKGGVAMLQQYFATAWI PHNDGTNNFYTANL 279
 T K+ K F +I N + ++ GWVAM+Q YF +AW+ ++ FYT +
 Sbjct: 233 PVVYTDASKFHKVDFKSIEKGNTEHDKTADNGWVAMVQHYFFSAWLHNDKAPREFYTRKI 292
 Query: 280 GNGIAAIGYKSQPVLVQPGQTGAMNSTLWVGPEIQDKMAAVAPHLDLTVDYGWLWFISQP 339
 + A+G + PG + +S L+VGP+ + K+ +AP L+L DYGW I++P
 Sbjct: 293 DVNLYAVGQLFPLGEIAPGASKQFDSVLFVGPQEEKKLETLAPGLELVKDYGWFTIIAKP 352
 Query: 340 LFKLLKWIHSFVGNWGFSSIIITFIVRGIMYPLTKAQYTSMAKMRMLQPKIQAMRERLGD 399
 LF LL +H +GNWG++I+ + +++ Y L Y SMAKM+ + PKI MRERL D
 Sbjct: 353 LFWLLDQLHKLIGNWGWAI VALVLLKAAFYWLNAKAYASMAKMKAINPKIMEMRERLKD 412
 Query: 400 DKQRISQEMMALYKAQKVNPLGGCFPLLIQMPIFLALYYMLMGSVELRQAPFALWIHDLS 459
 Q++ QEMM +YK EKVNPLGGC P+L+QMP+F+ALY++L+ SVE+R AP+ WI DLS
 Sbjct: 413 KPQQMQQEMMRYKEEKVNPLGGCLPILVQMPVFIALYWVLLSSVEMRNAPWLGWITDLS 472
 Query: 460 AQDPYYILPILMGVTMFFIQKMSPTTVDTPMQQKIMTFMPVIFTVFFLWFPGLVLYYIV 519
 +DP +ILPI+M T ++PT DPMQ K+M MP++F+V F +FP+GLVLY+I
 Sbjct: 473 VRDPLFILPIVMTGTLLQTWLNPTP-PDPMQAKMMWIMPLVFSVMFFFFPAGLVLYWIT 531
 Query: 520 SNLVTTIIQQQLIYRGL 535
 +NL++I QQ +I R L
 Sbjct: 532 NNLLSIAQQWVINRRL 547

>ref|ZP_00364739.1| COG0706: Preprotein translocase subunit YidC [Polaromonas sp.
 JS666]
 Length = 580

Score = 363 bits (931), Expect = 3e-99
 Identities = 199/493 (40%), Positives = 293/493 (59%), Gaps = 11/493 (2%)

Query: 43 AAGSAADQGVV---ASGQGLISVKTVDVLDLTINTRGGDVEQALLPAYPKELNSTQPFQL 99
 AA A G P A+ + + V TDVL LT ++ GG + + N+ F L
 Sbjct: 79 AAPGAVPAGAPSPAAAATRRVNVNTDVLALTFDSEGGTLVHSAFTRFKDMANTDAGFVL 138
 Query: 100 LETSPQFIYQAQSGLTGRDGPDPNANGPRPLYNVEKDAYVLAEGQNELQVPMTYTDAAGN 159
 L+ S +Y AQ+GL G + L V L +GQNELQV D G
 Sbjct: 139 LDESTNRVYVAQTGLIA-SGTGGTFPTHKTLMTVVPGERSLKDGQNELQVKFESADLGGV 197
 Query: 160 TFTKTFVLKRGDYAVNVNYNVQNAKEKPLEISSFGQLKQSITLPPHLDTGSSNFALHTFR 219
 KT+ LKRG Y + V ++V N G P+ + QL + PP G S+F TF
 Sbjct: 198 KLVKTYTLKRGSYDIAVRHDTVINTGSAPVAPQLYMLVLRDGNKPP-----GESSF-YSTFT 252
 Query: 220 GAAYSTPDEKEYEKYKFDTIADNE-NLNISSEKGGVAMLQQYFATAWI PHNDGTNNFYTAN 278
 G A T +KY+K +F I +N+ ++ + G+VAM+Q YFA AWI + + +
 Sbjct: 253 GPAIYTEAKKYQKVEFKDIENNKVDVEKQATNGYVAMVQHYFAAAWILADGLKRDLFRLK 312
 Query: 279 LGNGIAAIGYKSQPVLVQPGQTGAMNSTLWVGPEIQDKMAAVAPHLDLTVDYGWLWFISQ 338
 + + A+G + + PG T ++S L+VGP+ + K+ A+AP L+L DYGWL +++
 Sbjct: 313 VDANLYAVGLITPLDSIAPGATKTIDSRLVFGPQEEKKLEALAPGLELVKDYGWLTILAK 372
 Query: 339 PLFKLLKWIHSFVGNWGFSSIIITFIVRGIMYPLTKAQYTSMAKMRMLQPKIQAMRERLG 398
 PL+ LL +H F+ NWG+SI+ + +++ Y L Y SMAKM+ + PKI MRERL
 Sbjct: 373 PLYWLLDKLHGFLLNWGSIVALVLLKIAFYWLNAKAYASMAKMKAINPKIMEMRERLK 432

Query: 399 DDKQRISQEMMALYKAEKVNPLGGCFPLLIQMPIFLALYYMLMGSVELRQAPFALWIHDL 458
 D Q + Q MM +Y+ EKVNP+GGCFP+++Q+P+F+ALY++L+ SVE+R AP+ LWIHDL
 Sbjct: 433 DKPQEMQAMMKIYREEKVNPMGGCFPIMVQIPVFIALYWVLLSSVEMRNAPVWLWIHDL 492

Query: 459 SAQDPYYILPILMGVTMFFIQKMSPTTVTDPMQKIMTFMPVIFTVFFLWFPSGLVLYYI 518
 SA DP++ILP+LM +T ++P DPMQ K+M FMP+IF+V F +FP+GLVLY+I
 Sbjct: 493 SAPDPFFILPVLMTLTMTLQTALNPAP-PDPMQAKLMWFMPILFVSMFFFFFFPAGLVLYWI 551

Query: 519 VSNLVTIIQQQLI 531
 +N+++I QQ +I
 Sbjct: 552 TNNILSIAQQWVI 564

>ref|ZP_00211444.1| COG0706: Preprotein translocase subunit YidC [Burkholderia cepac
 R18194]
 Length = 538

Score = 362 bits (930), Expect = 3e-99
 Identities = 197/515 (38%), Positives = 303/515 (58%), Gaps = 28/515 (5%)

Query: 33 AQQTQTTTTA-----AGSAADQGV PASGQGKLISVKTDVLDLTINTRGGDVEQALLP 85
 A T TTTTA AG+A PA+ Q +L+ TDV D I+TRGG + + L
 Sbjct: 32 ASGTGATTTTAGEVPAAAAGAAPSTTAPAA-QAQLVKFSTDVYDGEIDTRGGTLAKLTLK 90

Query: 86 AYPKELNSTQP---FQLETS PQFIYQAQSGLTGRDGPDPNPANGPRPLYN-VEKDAYVLA 141
 K+ + QP L + + Y A+SGL G D P++ +Y + L
 Sbjct: 91 ---KQGDGKQPDLYITLFDHTAGHTYLARSGLLGDFPNH-----NDVYTQLNPGTTSLT 142

Query: 142 EGQNELQVPMTYTDAAGNTFTKTFVLKRGDYAVNVNYNVQNAKEKPLEISSFGQLKQSIT 201
 QN L++ G KT+ RG Y + V+ + N G P+ + + +L + T
 Sbjct: 143 GDQNALKLSFESPVKGGVKVVKTYTFTGRSYVIGVDTKIDNVGTAPVTPTVYMELVRDNT 202

Query: 202 LPPHLDTGSSNFALHTFRGAAYSTPDEKYEKYKFDTIADNE-NLNISSKGGWVAMLQQYF 260
 + HTF G A T + ++K F + N+ + S+ GWVAM+Q YF
 Sbjct: 203 AV-----ETPMFSHTFLGPAVYTDAKHQKINFSDLDKNKADYVTSADNGWVAMVQHYF 256

Query: 261 ATAWIPHNDGTNNFYTANLNGIAAIGYKSQPVLVQPGQTGAMNSTLWVGPEIQDKMAAV 320
 A+AWIP + Y + + +G K + PGQ+ + + L+ GPE + + +
 Sbjct: 257 ASAWIPQQGVKRDIIAEKIDPTLYRVGVKQPVAAIAPGQSADVQARLFAGPEEERMLEGI 316

Query: 321 APHLDLTVDYGWLWFI SQPLFKLLKWIHSFVGNWGFSSIIITFIVRGIMYPLTKAQYTSM 380
 AP L+L DYGW+ I++PLFLL+ IHS++GNWG+SI+++T +++ + +PL+ A Y SM
 Sbjct: 317 APGLELVKDYGWVTIIAKPLFWLLEKIHSYIGNWGSIVLLTLLIKAVFFPLSAASYKSM 376

Query: 381 AKMRMLQPKIQAMRERLGDDKQRISQEMMALYKAEKVNPLGGCFPLLIQMPIFLALYYML 440
 A+M+ + P++QA+RER D Q+++ +M LYK EKVNP GGC P++IQ+P+F++LY++L
 Sbjct: 377 ARMKEITPRMQALRERFKSDPQKMNSALMELYKTEKVNPFGGCLPVVIQIPVFISLYWVL 436

Query: 441 MGSVELRQAPFALWIHDL SAQDPYYILPILMGVTMFFIQKMSPTTVTDPMQKIMTFMPV 500
 + SVE+R AP+ LWIHDL +DP++ILP+LM V+M+ ++PT DP+Q K+M FMP+
 Sbjct: 437 LASVEMRGAPVWLWIHDL SQRDPFFILPVLMAVSMYVQTSLNPTP-PDPVQAKMMKFMP 495

Query: 501 IFTVFFLWFPSGLVLYYIVSNLVTIIQQQLIYRGL 535
 F+V F +FP+GLVLYY+V+N+++I QQ I R L
 Sbjct: 496 AFSVMFFFFFFPAGLVLYYVVNNVLSIAQQYYITRKL 530

>ref|NP_904074.1| integral membrane protein, 60 kDa [Chromobacterium violaceum ATCC

12472]
Length = 545

Score = 359 bits (921), Expect = 4e-98
Identities = 205/552 (37%), Positives = 317/552 (57%), Gaps = 30/552 (5%)

Query: 1 MDSQRNLLVIALLFVSFMI-WQAWEQDKN-PQPQAQQTQTQTTTTAAGSAADQGV PASGQG 58
MDS+R L++ LL V + W + K+ PQ QA +T TT A A +G
Sbjct: 1 MDSKR-LIIFVLLSVGILFGWNEYFMPKHTPQQQA AKTQATTGAANNVAQPADANKLTRG 59

Query: 59 KLISVKTDVLDLTINTRGGDVEQALLPAYPKELNSTQPFQ LLETSPQFIYQAQSGLTGRD 118
+ I VKTD+++ I+T GGD+ L + + QPFQL E S + +Y AQ+GL
Sbjct: 60 QRIQVKTDLVEAEIDTVGGDLRLSLKLLKHGAAEDHKQPFQLFEDSAKR VYVAQTGLVAAS 119

Query: 119 GPDNPANGPRPLYNVEKDAYVLAEGQNELQVPM TYTDAAGNTFTKT FVLKRGDYAVNVNY 178
P P + + ++ +K +Y L + L+V +T DA G +K + K+ Y + V Y
Sbjct: 120 NPALPTH--KTVFTSDKPSYQLTG--DTLEVKL TAPDANGVKVSKVYTFKKNSYEIGVRY 175

Query: 179 NVQNAGEKPLEISSFGQLKQSITLPPHLD TGSSNFALHTFRGAAYSTPDEKYEKYKFDTI 238
++ N G PL +++ +L + P G A HT+ G A T + K++K FD +
Sbjct: 176 DIVNGGAAPLAPTAYYRLLRDSQAPE----GEGRMA-HTYTGP AVYTSEHKFQKVSFDDL 230

Query: 239 ADNE-NLNISSKGGWVAMLQQYFATAWI PHN-DGTNNFY-----TANLGNGIAA 285
A + + ++ GWVAMLQ YF +AWI DG + TA L + A
Sbjct: 231 AKGKG DYAKTTT DGWVAMLQHYFMSAWILKPLDGASVCKDERS CRFELKETAGLNSAAAL 290

Query: 286 IGYKSQPVLVQPGQTGAMNSTLWVGPEIQDKMAAVAPHL DLTVDYGWLWFISQPLFKLLK 345
+ Y + V PG++ +++ L+ GPE + ++ +A ++ D+G + + PLF LL
Sbjct: 291 VDYAT----VAPGKSLSVSVPLYAGPEEYNI ISKLADGMEYAKDFGIFYIFASPLFWLLV 346

Query: 346 WIHSFVGNWGFSSIIITFIVRGIMYPLTKAQYTSMAKMRML QPKIQAMRERLGDDKQRIS 405
+H V NWG++I+++T V+ + YPLT A Y SMAKM+ L P+++ ++ + GDD+ +
Sbjct: 347 KLHGLVSNWGWAI VLLTTLTVKAVFYPLTAASYRSM AKMKALAPRLERLKAQHGD DRMKFQ 406

Query: 406 QEMMALYKA EKVNPLGGCFPLLIQMPIFLALY YMLMG SVELRQAPFALWIHDL SAQDPYY 465
Q +M +YK EKVNPLGGC P+LIQ+P+F+ LY+ L+ SVELR AP+ LW DL+ DPYY
Sbjct: 407 QAVMEMYKTEKVNPLGGCLPMLIQIPVFIGLYWALLASVELRGAPWVLWYTD LARPDPYY 466

Query: 466 ILPILMGVTMFFIQKMSPTT VTDPMQQKIMTFMPVIFTVFFLWFPSGLVLYYIVSNLVTI 525
ILP++M TMF ++P DPMQ K+M MP+ F+ F +FP+GLVLYY+V+N+++
Sbjct: 467 ILPVIMAATMFLQTFLNPPP-ADPMQAKMMKIMPLAFSAL FFFFPAGLVLYYVVNNVLSM 525

Query: 526 IQQQLIYRGLEK 537
QQ I + +EK
Sbjct: 526 AQQWFINKQIEK 537

>ref|ZP_00275894.1| COG0706: Preprotein translocase subunit YidC [Ralstonia
metallidurans CH34]
Length = 555

Score = 358 bits (919), Expect = 7e-98
Identities = 201/511 (39%), Positives = 306/511 (59%), Gaps = 20/511 (3%)

Query: 31 PQAQQTQTQTTTTAAGSAADQGV PASGQ--GKLISVKTDVLDLTINTRGGDVEQA-LLPAY 87
PQA T AA A+ Q G+ ++V TD + I+T GG + + LL +
Sbjct: 52 PQADV PKANATNAAPGTVPAAPQAAAQPVGEKVTVTTDEVRAEIDTAGGILSRLELLNEH 111

Query: 88 PKELNSTQPFQ LLETSPQFIYQAQSGLTGRD GPDNPANGPRPLYNVEKDAYVLAEGQNEL 147

K+ P LLE Y A+SGL G D P++ ++ V A LA GQ++L
 Sbjct: 112 EKD---GAPVLLERDVNRTYLARSLIGGDLNHTT-----VFTVAPGARTLAPGQDKL 163
 Query: 148 QVPMTYTDAGNTFTKTFVLKRGDYAVNVNYNVQNAGEKPLEISSFGQLKQSITLPPHLD 207
 V +T + G F KT+ +G Y V+ ++V N G + + + +L + +
 Sbjct: 164 DVVLT-AEKNQVGFVKTYTFHKGSYVVDTRFDVTNTGTAAVSPTLYLELARDGS-----K 217
 Query: 208 TGSSNFALHTFRGAAYSTPDEKYEKYKFDTIADNE-NLNISSKGGWVAMLQQYFATAWIP 266
 S F TF G A T +KY K F+ IA + + ++ GWVAM+Q YFA+AWIP
 Sbjct: 218 VEKSQF-YSTFTGPAIYTNADKYHKLTFEDIAKGGKATVPAATDNGWVAMVQHYFASAWIP 276
 Query: 267 HNDGTNNFYTANLNGIAAIGYKSQPVLVQPGQTGAMNSTLWVGPEIQDKMAAVAPHLDL 326
 ++FY + + +G + + PG T + ++ L+ GP+ + + + P L+L
 Sbjct: 277 QTGKQHSFYAEQIDPNLYRVGIQQPLGQLAPGATVSTDARLFAGPQEERMLEQITPGLLEL 336
 Query: 327 TVDYGWLWFIQSPLFKLLKWIHSFVGNWGSIIIIITFIVRGIMYPLTKAQYTSMAKMRML 386
 DYGWL +++PLF LL+ +H F+GNWG+SII +T +++ + +PL+ A Y SM KM+ L
 Sbjct: 337 VKDYGWLTILAKPLFWLLEKLHGFLGNWGSIIIGLTVLIKLVFFPLSAASYKSMGKMKDL 396
 Query: 387 QPKIQAMRERLGDDKQRISSQEMMALYKAEKVNPLGGCFPLLIQMPIFLALYYMLMGSVEL 446
 QP++ A+RER D Q+++QEMMALY+ EKVNPLGGC P++IQ+P+F+ALY++L+ SVE+
 Sbjct: 397 QPRMTAIRERHKGDPOKMNQEMMALYRTEKVNPLGGCLPIVIQIPVFIALYWVLLSSVEM 456
 Query: 447 RQAPFALWIHDLAQDPYYILPILMGVTMFFIQKMSPTTVTDPMQOKIMTEMPVIFTVFF 506
 R AP+ WIHDL DP+YILPI+M V+MF +++PT DP+Q K+M MP++F+ F
 Sbjct: 457 RGAPWLGIHDLSPDPFYILPIVMAVSMFVQTRLNPTP-PDPVQAKVMMIMPLVFSFMF 515
 Query: 507 LWFPGLVLYYIVSNLVTIIQQQLIYRGLEK 537
 +FP+GLVLY++V+N+++I QQ I R L K
 Sbjct: 516 FFFPAGLVLYWVNNILSIAQQWQINRMLGK 546

>ref|ZP_00219032.1| COG0706: Preprotein translocase subunit YidC [Burkholderia cepac
 R1808]
 Length = 537

Score = 358 bits (918), Expect = 9e-98

Identities = 201/545 (36%), Positives = 311/545 (57%), Gaps = 43/545 (7%)

Query: 18 MIQAWAQDKNPQ----PQAQQT-----TQTTTTA-----AGSAADQGV PAS 55
 M++ W++D P A QT T TTA AG+A PA+
 Sbjct: 1 MLYDNWQRDHGRPSMFFPSATQTAPAAASGASGTGATTTAGEAPAAAAAGAAPATTAPAA 60
 Query: 56 GQGLKISVKTDLVLDLTINTRGGDVEQALLPAYPKELNSTQP---FQLLETSPQFIYQAQS 112
 Q +L+ TDV D I+TRGG + + L K+ + QP L + + Y A++
 Sbjct: 61 -QAQLVKFSTDVYDGEIDTRGGTLAKLTLK---KQGDGKQPDLYITLFDHTAGHTY LART 116
 Query: 113 GLTGRDGPDPNPANGPRPLYN-VEKDAYVLAEGQNELQVPMTYTDAGNTFTKTFVLKRGD 171
 GL G D P++ +Y + A L QN L++ G KT+ RG
 Sbjct: 117 GLLGGDFPNH-----NDVYTQLNPGATSLTGDQNTLKLKSFESPVKGGVKVVKTYTFTRGS 171
 Query: 172 YAVNVNYNVQNAGEKPLEISSFGQLKQSITLPPHLDTGSSNFALHTFRGAAYSTPDEKYE 231
 Y + V+ + N G P+ + + +L + T + HTF G A T + ++
 Sbjct: 172 YVIGVDTKIDNVGTAPVTPTVYMEIVRDNTAV-----ETPMFSHTFLGPAVYTDKHFQ 225
 Query: 232 KYKFDTIADNENLNISSK-GGWVAMLQQYFATAWIPHNDGTNNFYTANLNGIAAIGYKS 290
 K F + N+ ++S GWVAM+Q YFA+AWIP + Y + + +G K
 Sbjct: 226 KINFSDLKDNKADYVNSADNGWVAMVQHYFASAWIPQQGVKRDYAEKIDPSLYRVGVKQ 285

Query: 291 QPVLVQPGQTGAMNSTLWVGPEIQDKMAAVAPHLDLTVDYGWLWFISQPLFKLLKWIHSF 350
 + PGQ+ + + L+ GPE + + +AP L+L DYGW+ I++PLF LL+ IH
 Sbjct: 286 PVAAIAPGQSADVQARLFAGPEEERMLEGIAPGLELVKDYGWVTIIAKPLFWLLEKIHGV 345

Query: 351 VGNWGFSSIIITFIVRGIMYPLTKAQYTSMAKMRMLQPKIQAMRERLGDDKQRISQEMMA 410
 VGNWG++I+++T +++ + +PL+ A Y SMA+M+ + P++QA+RER D Q+++ +M
 Sbjct: 346 VGNWGWAIVLLTILIKAVFFPLSAASYKSMARMKEITPRMQALRERFKSDPQKMNAALME 405

Query: 411 LYKAEKVNPLGGCFPLLIQMPIFLALYYMLMGSVELRQAPFALWIHDLSAQDPYYILPIL 470
 LYK EKVNP GGC P++IQ+P+F++LY++L+ SVE+R AP+ LWIHDLS +DP++ILP+L
 Sbjct: 406 LYKTEKVNPFGGCLPVVIQIPVFISLYWVLLASVEMRGAPWILWIHDLSQRDPFFILPVL 465

Query: 471 MGVTMFFIQKMSPTTVDPMQKIMTFMPVIFTVFFLWFPSGLVLYYIVSNLVTIIQQQL 530
 M V+M+ ++PT DP+Q K+M FMP+ F+V F +FP+GLVLYY+V+N+++I QQ
 Sbjct: 466 MAVSMYVQTSLNPTP-PDPVQAKMMKFMPIAFSVMFFFFPAGLVLYYVNNVLSIAQQYY 524

Query: 531 IYRGL 535
 I R L
 Sbjct: 525 ITRKL 529

>ref|NP_518125.1| PROBABLE TRANSMEMBRANE PROTEIN [Ralstonia solanacearum GMI1000]
 Length = 553

Score = 354 bits (908), Expect = 1e-96

Identities = 207/567 (36%), Positives = 315/567 (55%), Gaps = 56/567 (9%)

Query: 1 MDSQRNLLVIALLFVSFMIWQAWEQDKNPQQAQQTQTTTTAAGS----- 46
 MD +R +L + +++ W++ Q T QT TT A +
 Sbjct: 1 MDIKRTILWVIFSLSVLLFDNWQRANGHQSMFFPTPQTVTTTAAAPGGTPAGDVPKAAA 60

Query: 47 ---AADQGV PASGQ-----GKLISVKTDLVDLTINTRGGDVEQALLPAYPKELNSTQPF 97
 A Q PA+G + I V TDV+ T++T G V + L ++ + P
 Sbjct: 61 PAAAGSQAAPATGAVSQTPASEKIVVTTDVIRATVDTAGAIIVTK--LELLTQKDHDGNPM 118

Query: 98 QLLETSPQFIYQAQSGLTGRDGPDPNPANGPRPLYNVEKDAYVLAEGQNEL----QVPMY 153
 L + S + Y A+SGL G D P++ + + G +L +V +T
 Sbjct: 119 VLFDRSLERTYLARSLIGGDFPNHTT-----VFTASAGPRDLGTGGEVSLTL 166

Query: 154 T-DAAGNTFTKTFVLKRGDYAVNVNYNVQNAGEKPLEISSFGQLKQSITLPPHLDTS-- 210
 T D G KT+V KRG Y ++ ++V N G P+ + + +L + D G+
 Sbjct: 167 TADKGGAKLAKTYVFKRGSYVIDTRFDVTNDGAAPINPTLYMELAR-----DGGAVE 218

Query: 211 -SNFALHTFRGAAYSTPDEKYEKYKFDTIADNE-NLNISSKGGWVAMLQQYFATAWIPHN 268
 S F TF G A T + Y K F I ++ ++ + GWVAM+Q YFA+AWIP
 Sbjct: 219 QSRF-YSTFTGPAVYTDTDHYHKITFADIDKSKAHVPAPTDSGWVAMVQHYFASAWIPAA 277

Query: 269 DGTNNFYTANLNGIAAIGYKSQPVLVQPGQTGAMNSTLWVGPEIQDKMAAVAPHLDLTV 328
 FY + +G + V PG + + + L+ GP+ + + + P L+L
 Sbjct: 278 SAKREFYVDRIDTNFYRVGMQALGTVPAGASVSATARLFAGPQEERMLEGITPGLELVK 337

Query: 329 DYGWLWFISQPLFKLLKWIHSFVGNWGFSSIIITFIVRGIMYPLTKAQYTSMAKMRMLQ 388
 DYGWL I++PLF LL+ IH +GNWG+SI+ +T +V+ + +PL+ Y SMAKM+ LQP
 Sbjct: 338 DYGWLTIIAKPLFWLLEKIHKLGNWGSIVALTVLVKLVFFPLSATSYSMAKMKDLQP 397

Query: 389 KIQAMRERLGDDKQRISQEMMALYKAEKVNPLGGCFPLLIQMPIFLALYYMLMGSVELRQ 448
 ++ A+RER D Q+++QEMM LY+ EKVNPGLGC P++IQ+P+F+ALY++L+ SVE+R
 Sbjct: 398 RMTAIRERHKGDPOKMNQEMMTLYRTEKVNPLGGCLPIVIQIPVFIALYWVLLSSVEMRG 457

Query: 449 APFALWIHDLAQDPYYILPILMGVTMFFIQKMSPTTVTDPMQQKIMTFMPVIFTVFFLW 508
 AP+ W+HDL++ DP+YILPILM V+MF +++PT DP+Q K+M FMP+ F+V F +
 Sbjct: 458 APWLGWVHDLASPDPFYILPILMAVSMFVQTRLNPTP-PDPVQAKMMMFMPIAFSVMFFF 516

Query: 509 FPSGLVLYYIVSNLVTIIQQQLIYRGL 535
 FP+GLVLY++V+N ++I QQ I R L
 Sbjct: 517 FPAGLVLYWVNNCLSLIAQQWSINRML 543

>ref|ZP_00167342.2| COG0706: Preprotein translocase subunit YidC [Ralstonia eutropha
 JMP134]
 Length = 555

Score = 353 bits (907), Expect = 2e-96
 Identities = 202/514 (39%), Positives = 302/514 (58%), Gaps = 30/514 (5%)

Query: 31 PQAQQTQTQTTTTAAGSAADQGVPSAGQKGLISVKTDVLDLTINTRGGDVEQA-LLPAYPK 89
 P+A T AA A Q A G+ I V TD + I+T GG + + LL + K
 Sbjct: 56 PKANATAGAAAPAAPGGAPQAA-AQPTGEKIIIVTTDEVRAEIDTAGGILSRLELLNEHEK 114

Query: 90 ELNSTQPFQLETSPQFIYQAQSGLTGRDGPDPNPA-----NGPRPLYNVEKDAYVLAEGQ 144
 + +P L E Y A+SGL G D P++ GPR L +G
 Sbjct: 115 D---GKPVVLFERDTRTYMARSGLIGGDLPNHTTVFTATPGPRTL-----DGA 160

Query: 145 NELQVPMTYTDAGNTFTKTFLVLRGDIYAVNVNYNVQNAGEKPLEISSFGQLKQSITLPP 204
 ++L+V +T D G F KT+V +G Y V+ + V N G P+ + +L+ +
 Sbjct: 161 DKLEVTLT-ADKNGVKFVKTYVFHKGSIYVVDARFAVTNDGTAPVSPTLYMELARDGS--- 216

Query: 205 HLDTGSSNFALHTFRGAAYSTPDEKEYEKYKFDTIADNE-NLNISSKGGWVAMLQOYFATA 263
 S F T F G A T +KY K F D I A + + ++ GWVAM+Q YFA+A
 Sbjct: 217 --KVEQSQF-YSTFTGPAIYTDADKYHKITFDDIAKGKASTPAATTSGWVAMVQHYFASA 273

Query: 264 WIPHNDGTNNFYTANLNGIAAIGYKSPVLVQPGQTGAMNSTLWVGPEIQDKMAAVAPH 323
 WIP ++FY + + +G + + PG T ++ L+ GP+ + + + P
 Sbjct: 274 WIPQAGKEHSFYVQQIDPNLYRVGIQQPLGQIAPGATVTTDARLFAGPQEERMLEKITPG 333

Query: 324 LDLTVDYDGLWLFISQPLFKLLKWIHSFVGNWGFSSIIITFIVRGIMYPLTKAQYTSMAKM 383
 L+L DYGLW +++PLF LL+ +H F+ NWG+SII +T +++ + +PL+ A Y SM KM
 Sbjct: 334 LELVKDYGWLTILAKPLFWLLEKLHGFLNNWGSIIALTVLIKLVFFPLSAASYKSMGKM 393

Query: 384 RMLQPKIQAMRERLGGDKQRISQEMMALYKAQKVNPLGGCFPLLIQMPIFLALYYMLMGS 443
 + LQP++ ++RER D Q+++ EMMALYK EKNVPLGGC P++IQ+P+F+ALY++L+ S
 Sbjct: 394 KDLQPRMTSIRERHKGDPQKMNAEMMALYKTEKNVPLGGCLPIVIQIPVFIALYWVLLSS 453

Query: 444 VELRQAPFALWIHDLAQDPYYILPILMGVTMFFIQKMSPTTVTDPMQQKIMTFMPVIFT 503
 VE+R AP+ WIHDL DP+YILPI+M V+MF +++PT DP+Q K+M MP++F+
 Sbjct: 454 VEMRGAPWLGWIHDLSPDPFYILPIVMAVSMFVQTRLNPTP-PDPVQAKVMMIMPLVFS 512

Query: 504 VFFLWFPSGLVLYYIVSNLVTIIQQQLIYRGLEK 537
 F +FP+GLVLY++V+N+++I QQ I R L K
 Sbjct: 513 FMFFFFPAGLVLYWVNNILSLIAQQWQINRMLGK 546

>ref|NP_644666.1| 60 kDa inner-membrane protein [Xanthomonas axonopodis pv. citri
 str. 306]
 Length = 574

Score = 345 bits (884), Expect = 8e-94

Identities = 214/572 (37%), Positives = 305/572 (53%), Gaps = 43/572 (7%)

Query: 1 MDSQRNLLVIALLFVSMIWAWEQDK-----NPQPQAQQTQTQTTTTAAGSAAD 49
 M+ R L+ A L V+ ++W W +DK P A+ T +AA A

Sbjct: 1 MNQTRVFLIFAWLMVAALLWMEWGDKAAANAPVVAATQSVPAARDLDAATPSAANVPAA 60

Query: 50 QGVP-----ASGQGLISVKTDVLDLTINTRGGDVEQALLPAYPKE 90
 Q +P A+G ++++ +DVL L ++ G V A L +P+

Sbjct: 61 QAIPQAGAPGAVPATSTTAATPAAAGAAPVVTLTSDVLRCLKD--GRSVLDAELLQFPQT 118

Query: 91 LNSTQPFQLETSPOFIYQAQSGLTGRDGPDPNANGPRPLYNVEKDAYVLAEGQNELQVP 150
 + T P LL P Y A SG P G R + +A+GQN L VP

Sbjct: 119 KDGTA PVSLLTEDPAHPYNATSGWASEHSPVPGVGGFRA--EQPGTTFDMAKQNTLVVP 176

Query: 151 MTYTDAAGNTFTKTFVLKRGDYAVNVNYNVQNAGEKPLEISSFGQLKQSITLPPHLD TGS 210
 + G + +TF L+RG YA+++ V N P F +L + +P L G

Sbjct: 177 FVWNGPDGVSIRRTFTLERGRYAISIKDEVINKSGAPWNGYVFRKLSR---VPTILSRGM 233

Query: 211 SNFALHTFRGAAYSTPDEKEYEKYKFDTIADNENLNISCKGGWVAMLQQYFATAWIPHN DG 270
 +N +F GA + +P E YE+ F D+ LN GGWVA+LQ +F TAWIP D

Sbjct: 234 TNPDSFSFNGATWYSPQEGYERRAFKDYMDGGGLNRQITGGWVALLQHFFFTAWIPQKDQ 293

Query: 271 TNNFYTANLNGIAAIGYKSQPVLVQPGQTGAMNSTLWVGPEIQDKMAAV-APHLDLTVD 329
 + + A G A + V PGQT + + LWVGP++ +A LD VD

Sbjct: 294 ASLYVLAQDGRDVA-ELRGPATTVAPGQTASTEARLWVGPKLVSLIAKEDVKGLDRVVD 352

Query: 330 YGW---LWFISQPLFKLLKWIHSFVGNWGFSSIIITFIVRGIMYPLTKAQYTSMAKMRML 386
 Y + I Q LF +L +HSF+ NWG++II + ++R +YPL+ AQY S AKMR

Sbjct: 353 YSRFSIMAIIGQLFWVLSHLHSFLHNWGWAIIGLVLLRLALYPLSAAQYKSGAKMRRF 412

Query: 387 QPKIQAMRERLGGDKQRISQEMMALYKAEKVNPLGGCFPLLIQMPIFLALYYMLMG SVEL 446
 QP++ ++ER GDD+ + Q M L+K EK+NP+GGC PLLIQMPIF ALY++L+ SVEL

Sbjct: 413 QPRLAQLKERYGDDRKYQQATMELFKKEKINPMGGCLPLLIQMPIFFALYWVLVESVEL 472

Query: 447 RQAPFALWIHDLAQDPYYILPILMGVTMFFIQKMSPTTVDTPMQQKIMTFMPVIFTVFF 506
 RQAP+ WI DL+A+DPY+ILP+L M+ QK++PT DPMQ K+M FMP++F V

Sbjct: 473 RQAPWLGIQDLTARDPYFILPLLNISIMWATQKLTPTPGMDPMQAKMMQFMPLVFGVMM 532

Query: 507 LWFPGLVLYYIVS-NLVTIIQQQLIYRGLEK 537
 + P+GLVLY++V+ L +IQ +I + EK

Sbjct: 533 AFMPAGLVLYWVVGGLGLLIQWWMIRQHGEK 564

>ref|NP_639574.1| 60kDa inner-membrane protein [Xanthomonas campestris pv. campestris str. ATCC 33913]
 Length = 573

Score = 339 bits (869), Expect = 4e-92

Identities = 211/571 (36%), Positives = 302/571 (52%), Gaps = 42/571 (7%)

Query: 1 MDSQRNLLVIALLFVSMIWAWEQDKN----PQPQAQQTQTQTTTTAAGSAADQGV PAS- 55
 M+ R L+ A L V+ ++W W +DK P P A Q +A VP++

Sbjct: 1 MNQTRVFLIFAWLMVAALLWMEWGDKAAANAPTPIASQAVPAARDPDAAAPAANVPSAQ 60

Query: 56 -----GQGKLISVKTDVLDLTINTRGGDVEQALLPAYPKEL 91
 G I++ +DVL L ++ G V A L +P+

Sbjct: 61 AIPQAGSPAAPATSTTTATPATTGAAPAITLTSDVLRCLKD--GRSVLDAELLQFPQTK 118

Query: 92 NSTQPFQLETSPOFIYQAQSGLTGRDGPDPNANGPRPLYNVEKDAYVLAEGQNELQVPM 151

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      + T+P +LL      Y A SG      P      G R      + LA+GQN L VP
Sbjct: 119 DGTEPVKLLTEDAAHPYNATSGWASERSPVPGVGGFRA--EQPGTTFELAKGQNTLVVPF 176

Query: 152 TYTDAAGNTFTKTFVLKRGDYAVNVNYNVQNAGEKPLEISSFGQLKQSITLPPHLDTGSS 211
      +      G +      + F L+RG YA+++ V N +      F +L +      +P L G +
Sbjct: 177 VWNGPNGVSIRRIFTLQGRSYAISIKDEVINKSDAAWNGYVFRKLSR---VPTILSRGMT 233

Query: 212 NFALHTFRGAAYSTPDEKYEKYKFDTIADNENLNISKGGWVAMLQQYFATAWIPHNDGT 271
      N      +F GA + +P E YE+ F      D+ LN      GGWVA+LQ +F TAWIP D
Sbjct: 234 NPDSFSFNGATWYSPQEGYERRAFKDYMDGGGLNRQITGGWVALLQHFFFTAWIPQKDQA 293

Query: 272 NNFYTANLGNIAAIGYKSQPVLVQPGQTGAMNSTLWVGPEIQDKMAAV-APHLDLTVDY 330
      + + A G      A +      V PGQ+ + + LWVGP++ +A      LD VDY
Sbjct: 294 SLYVLAQDGPDRV-ELRGPAFTVAPGQSASTEARLWVGPKLVSLAKEDVKGLDRVVDY 352

Query: 331 GW---LWFISQPLFKLLKWIHSFVGNWGFSSIIITFIVRGIMYPLTKAQYTSMAKMRMLQ 387
      + I Q LF +L +HSF+ NWG++II +      ++R +YPL+ AQY S AKMR Q
Sbjct: 353 SRFSIMAIIGQLFWVLSHLHSFLHNWGWAIIGLVVLLRLALYPLSAAQYKSGAKMRRFQ 412

Query: 388 PKIQAMRERLGDDKQRISQEMMALYKAQKVNPLGGCFPLLIQMPIFLALYYMLMGVSVELR 447
      P++ ++ER GDD+Q+ Q M L+K EK+NP+GGC PLLIQMPIF ALY++L+ SVELR
Sbjct: 413 PRLAQLKERYGDDRQKYQQATMELFKKEKINPMGGCLPLLIQMPIFFALYWVLVESVELR 472

Query: 448 QAPFALWIHDLAQDPYYILPILMGVTMFFIIQKMSPTTVTDPMQKIMTFMPVIFTVFFL 507
      QAP+ WI DL+A+DPY+ILP+L M+ QK++PT DPMQ K+M FMP++F V
Sbjct: 473 QAPWLGIQDLTARDPYFILPVLNIAIMWATQKLTPTPGMDPMQAKMMQFMPLVFGVMMMA 532

Query: 508 WFPSGLVLYYIVS-NLVTIIQQQLIYRGLEK 537
      + P+GLVLY++V+ L +IQ +I + EK
Sbjct: 533 FMPAGLVLYWVVGGLGLLIQWWMIRQHGEK 563

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>ref|NP_283364.1| putative integral membrane protein [Neisseria meningitidis Z2491]
Length = 545

Score = 331 bits (849), Expect = 9e-90

Identities = 189/558 (33%), Positives = 293/558 (52%), Gaps = 41/558 (7%)

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Query: 1 MDSQRNLLVIALLFVSFMIWQAWEQDKNPQPAQQTQTQTTTTAAGSAADQGV PASGQGL 60
      MD +R      A+ V + W+      P P QQT Q      A + A      A
Sbjct: 1 MDFKRLTAFFAIALVIMIGWEKMFPTPKVPAPQQTAAQQQAVTASAEA-----ALAPATP 55

Query: 61 ISVKTDVLDLTINTRGGDVEQALLPAYPKELNSTQPFQLETSQPFYIQAQSGLTGRDGP 120
      I+V TD + I+ + GD+ + L Y + +PF L      ++ Y AQS L      G
Sbjct: 56 ITVTDTVQAVIDEKSGDLRRLTLLKYKATGDENKPFILFGDGKEYTYVAQSELLDAQG- 114

Query: 121 DNPANG-----PRPLYNVEKDAYVLAEGQNELQVPMTYTDAAGNTFTKTFVLKRGDYAVN 175
      +N G      P+ Y++E D      +++V ++ + G      K + +G Y VN
Sbjct: 115 NNILKGIGFSAPKKQYSLEGD-----KVEVRLSAPETRGLKIDKVYTFTKGSYLVN 165

Query: 176 VNYNVQNAGEKPLEISSFGQLKQSITLPPHLDTGSSNFALHTFRGAAYSTPDEKYEKYKF 235
      V +++ N + +S+ ++ +      H +      + H++ G      TP+ ++K F
Sbjct: 166 VRFDIANGSGQTANLSADYRIVRD-----HSEPEGQGYFTHSYVGPVVYTPEGNFQKVVSF 220

Query: 236 DTIADNENLNIS-----SKGGWVAMLQQYFATAWIPHNDGTNNFYTAN-----LG 280
      + D+      S      + GW+ M++ +F + WI      G + A
Sbjct: 221 SDLDDDAKSGKSEA EYIRKTPTGWLGMIEHHFMSTWILQPKGGQSVCAAGDCRIDIKRN 280

Query: 281 NGIAAIGYKSQPVLVQPGQTGAMNSTLWVGPEIQDKMAAVAPHLDLTVDYGWLWFISQPL 340

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Sbjct: 281 + + + +Q G + L+ GP+ +A +A +L L DYG + + + PL
DKLYSTSVSVPLAAIQNGAKSEASINLYAGPQTTSVIANIADNLQLAKDYGKVHWFASPL 340

Query: 341 FKLLKWIHSFVGNWGFSSIIITFIVRGIMYPLTKAQYTSMAKMRMLQPKIQAMRERLGDD 400
F LL +H+ +GNWG++II++T IV+ ++YPLT A Y SMAKMR PK+QA++E+ GDD

Sbjct: 341 FWLLNQLHNIIGNWGWAIIVLTIIVKAVLYPLTNASYRSMAMRAAAPKLQAIKEKYGDD 400

Query: 401 KQRISQEMMALYKAEKVNPLGGCFPLLIQMPIFLALYYMLMGVELRQAPFALWIHDLA 460
+ Q MM LY EK+NPLGGC P+L+Q+P+F+ LY+ L SVELRQAP+ WI DLS

Sbjct: 401 RMAQQQAMMQLYTDEKINPLGGCLPMLLQIPVFIGLYWALFASVELRQAPWLGWITDLR 460

Query: 461 QDPYYILPILMGVTMFFIQKMSPTTVTDPMQKIMTFMPVIFTVFFLWFPSGLVLYYIVS 520
DPYYILPI+M TMF ++P TDPMQ K+M MP++F+V F +FP+GLVLY++++

Sbjct: 461 ADPPYYILPIIAMAATMFAQTYLNPFP--TDPMAKMMKIMPLVFSVMFFFFPAGLVLYWVIN 519

Query: 521 NLVTIIQQQLIYRGLEKR 538
NL+TI QQ I R +EK+

Sbjct: 520 NLLTIAQQWHINRSIEKQ 537

>ref|NP_274901.1| 60 kd inner-membrane protein [Neisseria meningitidis MC58]
Length = 545

Score = 330 bits (847), Expect = 1e-89

Identities = 190/558 (34%), Positives = 292/558 (52%), Gaps = 41/558 (7%)

Query: 1 MDSQRNLLVIALLFVSMIWAQWEQDKNPQPAQQTQTTTTAAGSAADQGVPSAGQGKL 60
MD +R A+ V + W+ P P QQ Q A + A A

Sbjct: 1 MDFKRRLTAFFAIALVIMIGWEKMFPTPKPVPAQQAQQAQVTA SAEA-----ALAPATP 55

Query: 61 ISVKTDVLDLTINTRGGDVEQALLPAYPKELNSTQPFQLETSQFIIYQAQSGLTGRDGP 120
I+V TD + I+ + GD+ + L Y + +PF L ++ Y AQS L G

Sbjct: 56 ITVTDTTVQAVIDEKSGDLRRLTLLKYKATGDENKPFILFGDGKEYTYVAQSELLDAQG- 114

Query: 121 DNPANG-----PRPLYNVEKDAYVLAEGQNELQVPMTYTDAAGNTFTKTFVLKRGDYAVN 175
+N G P+ Y++E D +++V ++ + G K + +G Y VN

Sbjct: 115 NNILKGIGFSAPKKQYSLEGD-----KVEVRLSAPETRGLKIDKVYTFTKGSYLVN 165

Query: 176 VNYNVQNAGEKPLEISSFGQLKQSITLPPHLDTGSSNFALHTFRGAAYSTPDEKYEKYKF 235
V +++ N + +S+ ++ + H + + H++ G TP+ ++K F

Sbjct: 166 VRFDIANGSGQTANLSADYRIVRD-----HSEPEGQGYFTHSYVGPVVYTPEGNFQKVSF 220

Query: 236 DTIADNENLNIS-----SKGGWVAMLQQYFATAWIPHNDGTNNFYTANLGN----- 281
+ D+ S + GW+ M++ +F + WI G + A N

Sbjct: 221 SDLDDDAKSGKSEA EYIRKTP TGLWGMIEHHFMSTWILQPKGRQSVCAAGECNIDIKRRN 280

Query: 282 -GIAAIGYKSQPVLVQPGQTGAMNSTLWVGPEIQDKMAAVAPHLDTVDYGWLWLFISQPL 340
+ + +Q G + L+ GP+ +A +A +L L DYG + + + PL

Sbjct: 281 DKLYSTSVSVPLAAIQNGAKAEASINLYAGPQTTSVIANIADNLQLAKDYGKVHWFASPL 340

Query: 341 FKLLKWIHSFVGNWGFSSIIITFIVRGIMYPLTKAQYTSMAKMRMLQPKIQAMRERLGDD 400
F LL +H+ +GNWG++II++T IV+ ++YPLT A Y SMAKMR PK+QA++E+ GDD

Sbjct: 341 FWLLNQLHNIIGNWGWAIIVLTIIVKAVLYPLTNASYRSMAMRAAAPKLQAIKEKYGDD 400

Query: 401 KQRISQEMMALYKAEKVNPLGGCFPLLIQMPIFLALYYMLMGVELRQAPFALWIHDLA 460
+ Q MM LY EK+NPLGGC P+L+Q+P+F+ LY+ L SVELRQAP+ WI DLS

Sbjct: 401 RMAQQQAMMQLYTDEKINPLGGCLPMLLQIPVFIGLYWALFASVELRQAPWLGWITDLR 460

Query: 461 QDPYYILPILMGVTMFFIQKMSPTTVTDPMQKIMTFMPVIFTVFFLWFPSGLVLYYIVS 520

DPYYILPI+M TMF ++P TDPMQ K+M MP++F+V F +FP+GLVLY++V+
 Sbjct: 461 ADPPYILPII MAATMFAQTYLNPPP-TDPMQAKMMKIMPLVFSVMFFFFPAGLVLYWVVN 519

Query: 521 NLVTIIQQQLIYRGLEKR 538

NL+TI QQ I R +EK+

Sbjct: 520 NLLTIAQQWHINRSIEKQ 537

>ref|NP_780291.1| 60 kDa inner-membrane protein [Xylella fastidiosa Temecula1]
 Length = 565

Score = 329 bits (843), Expect = 4e-89

Identities = 206/571 (36%), Positives = 313/571 (54%), Gaps = 30/571 (5%)

Query: 1 MDSQRNLLVIALLFVSFMIWQAEQDKNPQPAQQTQTTTT-----AGSAA 48
 M+ R LL+ + L V+ ++W W ++KN + + + AG+
 Sbjct: 1 MNQTRVLLIFSWLTVATLLWMDWSKNKNETLEISASHNLGVDSNLELEHAVPQIHAGAVP 60

Query: 49 -----DQGPASGQGLISVKTDVLDLTINTRGGDVEQALLPAYPKELN-STQPFQLETS 103
 Q + A+ + +I+V TDVL L ++ G + A L +P+ + +P +LL

Sbjct: 61 LQKDSQLIAAAPKVPVINVTDDVLQKLDD--GFSILAADLLRFPQSKDRGAKPIKLLTDD 118

Query: 104 PQFIYQAQSGLTGRDGPDPNPANGPRPLYNVEKDAYVLAEGQNELQVPMTYTDAAGNTFTK 163
 P + Y A +G + P N L +Y LA QN L VP +T A G + +

Sbjct: 119 PNYPYSATTGWVSQSNPVP-NLSTFLPEQPDVSYKLANDQNRLVVPFIWTAANGVSIRR 177

Query: 164 TFVLKRGDYAVNVNYNVQNAGEKPLEISSFGQLKQSITLPPHLDTGSSNFALHTFRGAAY 223
 TF +RG YA+ + ++N+GE P F +L + + +P L+ +N +F GA +

Sbjct: 178 TFTFERGRYAILIRDEIRNSGETPWNAYVFRKLSR-VPIPNILNRAMTNPDSFSFNGAVW 236

Query: 224 STPDEKYEKYKFDTIADNENLNISSKGGWVAMLQOYFATAWIPHNDGTNNFYTANLNGI 283
 + YE+ F ++ LN GGW+A+LQ +F TAWIP D + + A NG

Sbjct: 237 YSEKGGYERRAFKDYMNDDGLNREIGGGWIALQLHHFFTAWIPQKDQASLYLLAQ--NGS 294

Query: 284 AAIGYKSQPVL-VQPGQTGAMNSTLWVGPEIQDKMAAV-APHLDLTVDYG---WLWFISQ 338
 I P V PGQT + LWVGP++ +++ LD VDY + I Q

Sbjct: 295 RDIAELRGPAFTVAPGQTTTTTEARLWVGPKLVEQITKEHVKGLDRVVDYSRFLMALIGQ 354

Query: 339 PLFKLLKWIHSFVGNWGFSSIIITFIVRGIMYPLTKAQYTSMAKMRMLQPKIQAMRERLG 398
 LF +L ++S + NWG++I+ + ++R MYPL+ +QY S AKMR QP++Q ++ER G

Sbjct: 355 GLFWILSHLNSLLHNWGWAIWGLVLLRIAMYPLSASQYKSAKMRKFQPRQLQLKERYG 414

Query: 399 DDKQRISQEMMALYKAEKVNPLGGCFPLLIQMPIFLALYYMLMGSVELRQAPFALWIHDL 458
 +D+Q+ Q MM LYK EK+NP+GGCFP+LIQMPIF ALY++L+ SVELRQAP+ WI DL

Sbjct: 415 EDRQKFQQAMMELYKKEKINPMGGCFPILIQMPIFFALYWVLVESVELRQAPWLGIQDL 474

Query: 459 SAQDPYYILPILMGVTMFFIQKMSPTTV-TDPMQQKIMTFMPVIFTVFFLWFPGLVLYY 517
 + +DPY+ILP+L V M+ QK++PT DP+ K+M MP+IF V + PSGL LY+

Sbjct: 475 TTRDPYFILPLLNIWIMWATQKLTPTPAGMDPIAGKMMQVMPLIFGVMAFVPSGLALYW 534

Query: 518 IVS-NLVTIIQQQLIYRGLEKRLHSREKKK 547

+++ L +IQ +I + + SRE K

Sbjct: 535 VINGGLNLLIQWWMIRQHADFSSRSRENIK 565

>ref|ZP_00042125.1| COG0706: Preprotein translocase subunit YidC [Xylella fastidiosa
 Ann-1]
 Length = 565

Score = 328 bits (841), Expect = 7e-89

Identities = 206/571 (36%), Positives = 313/571 (54%), Gaps = 30/571 (5%)

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Query: 1  MDSQRNLLVIALLFVSFMIWQAWQDKNPQQAQQTQTTTTA-----AGSAA 48
      M+  R LL+ + L V+ ++W  W ++KN  +  +  +  AG+
Sbjct: 1  MNQTRVLLIFSWLTVATLLWMDWGKKNKNETLEISASHNLGVDSNLELEHAVPQINAGAVP 60

Query: 49  ----DQGV PASGQGKLISVKTDVLDLTINTRGGDVEQALLPAYPKELN-STQPFQ LLETS 103
      Q + A+ + +I+V TDVL L ++ G + A L +P+ + +P +LL
Sbjct: 61  LQKDSQLIAAAPKVPVINVTDLVLQKLD--GFSILAADLLRFPQSKDRGAKPIKLLTDD 118

Query: 104 PQFIYQAQSGLTGRDGPDPNANGPRPLYNVEKDAYVLAEGQNELQVPMTYTDAAGNTFTK 163
      P + Y A +G + P N L +Y LA QN L VP +T A G + +
Sbjct: 119 PNYPY SATTGWVSQSNPVP-NLSTFLPEQPDVSYKLANDQNRLVVPFVWTAANGVSIRR 177

Query: 164 TFLVKRGDYAVNVNYNVQNAKEKPLEISSFGQLKQSITLPPHLDTGSSNFALHTFRGAAY 223
      TF +RG YA+ + ++N+GE P F +L + + +P L+ +N +F GA +
Sbjct: 178 TFTFERGRYAILIRDEIRNSGETPWNAYVFRKLSR-VPIPNILNRAMTNPDSFSFNGAVW 236

Query: 224 STPDEKYEKYKFDTIADNENLNISSKGGWVAMLQQYFATAWIPHNDGTNNFYTANLNGNI 283
      + YE+ F ++ LN GGW+A+LQ +F TAWIP D + + A NG
Sbjct: 237 YSEKGGYERRAFKDYMNDDGGLNREIGGGWIALQLHHFFTAWIPQKDQASLYLLAQ--NGS 294

Query: 284 AAIGYKSQPVL-VQPGQTGAMNSTLWVGPEIQDKMAAV-APHLDLTVDYG---WLWFISQ 338
      I P V PGQ+ + LWVGP++ +++ LD VDY + I Q
Sbjct: 295 RDIAELRGPAFTVAPGQSTTTEARLWVGPKLVEQITKEHVKGGLDRVVDYSRFQLMALIGQ 354

Query: 339 PLFKLLKWIHSFVGNWGFSSIIITFIVRGIMYPLTKAQYTSMAKMRMLQPKIQAMRERLG 398
      LF +L ++S + NWG++I+ + ++R MYPL+ AQY S AKMR QP++Q ++ER G
Sbjct: 355 GLFWILSHLNSLLHNWGWAIWGLVLLRIAMYPLSAAQYKSAKMRKFQPRQLQKERYG 414

Query: 399 DDKQRISQEMMALYKAEKVNPLGGCFPLLIQMPIFLALYYMLMGVSVELRQAPFALWIHDL 458
      +D+Q+ Q MM LYK EK+NP+GGCFP+LIQMPIF ALY++L+ SVELRQAP+ WI DL
Sbjct: 415 EDRQKFQQAAMELYKKEKINPMGGCFPILIQMPIFFALYWVLVESVELRQAPWLGIQDL 474

Query: 459 SAQDPYYILPILMGVTMFFIQKMSPTTV-TDPMQQKIMTFMPVIFTVFFLWFPSGLVLYY 517
      + +DPY+ILP+L V M+ QK++PT DP+ K+M MP+IF V + PSGL LY+
Sbjct: 475 TTRDPYFILPLLNIWIMWATQKLTPTPAGMDPIAGKMMQVMPLIFGVMMAFVPSGLALYW 534

Query: 518 IVS-NLVTIIQQQLIYRGLEKRGHLSREKKK 547
      +++ L +IQ +I + + SRE K
Sbjct: 535 VINGGLNLLIQWWMIRQHADF SRKRSRENIK 565

```

>ref|NP_300057.1| 60kDa inner-membrane protein [Xylella fastidiosa 9a5c]
Length = 565

Score = 328 bits (840), Expect = 1e-88

Identities = 201/557 (36%), Positives = 304/557 (54%), Gaps = 31/557 (5%)

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Query: 1  MDSQRNLLVIALLFVSFMIWQAWQDKNPQQAQQTQTTTTAAGSAADQGV PASGQGKL 60
      M+  R LL+ + L V+ ++W  W ++KN  +  +Q  +  + VP G +
Sbjct: 1  MNQTRVLLIFSWLTVATLLWMDWGKKNKNETLEIS-ASQNLGVDSNLELEHAVPQINAGAV 59

Query: 61  -----ISVKTDVLDLTINTRGGDVEQALLPAYPKELN-STQPFQ LLET 102
      I+VKTDVL L ++ G V A L +P+ + +P +LL
Sbjct: 60  PVQKDSQLIAVAPKVPVINVKTDVVLQKLD--GFSVLAADLLRFPQSKDRGAKPIKLLTD 117

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Query: 103 SPQFIYQAQSGLTGRDGPDPNPANGPRPLYNVEKDAYVLAEGQNELQVPMTYTDAAGNTFT 162
 P + Y A + G + P N L + Y LA Q+ L VP + T A G +
 Sbjct: 118 DPNYPYSATTGWVSQSNPVP-NLSTFLPEQPGVSYKLANDQDRLVVPFVWTAANGVSIR 176

Query: 163 KTFVLKRGDYAVNVNYNVQNAGEKPLEISSFGQLKQSITLPPHLDTGSSNFALHTFRGAA 222
 +TF +RG YA+ + ++N GE P F +L + + +P L+ +N +F GA
 Sbjct: 177 RTFTFERGRYAILIRDEIRNGGETPWNAYVFRKLSR-VPIPNILNRAMTNPDSFSFNGAV 235

Query: 223 YSTPDEKYEKYKFDTIADNENLNISSEKGGWVAMLQQYFATAWIPHNDGTNNFYTANLGNG 282
 + + YE+ F ++ LN GGW+A+LQ +F TAWIP D + + A NG
 Sbjct: 236 WYSEKGGYERRAFKDYMNDDGGLNREIGGGWIALLOHHFFTAWIPQKDQASLYLLAQ--NG 293

Query: 283 IAAIGYKSQPV-LVQPGQTGAMNSTLWVGPEIQDKMAAV-APHLDLTVDYG---WLWFIS 337
 I P V PGQ+ + LWVGP++ +++ LD VDY + I
 Sbjct: 294 SRDIAELRGPAFTVAPGQSTTEARLWVGPKLVEQITKEHVKGGLDRVVDYSRFLMALIG 353

Query: 338 QPLFKLLKWIHSFVGNWGFSSIIITFIVRGIMYPLTKAQYTSMAKMRMLQPKIQAMRERL 397
 Q LF +L ++S + NWG++I+ + ++R MYPL+ AQY S AKMR QP++Q ++ER
 Sbjct: 354 QGLFWILSHLNSLLHNWGWAIWGLVLLRIAMYPLSAAQYKSAKMRKFQPRLOQLKERY 413

Query: 398 GDDKQRISQEMMALYKAQKVNPLGGCFPLLIQMPIFLALYYMLMGSSVELRQAPFALWIHD 457
 G+D+Q+ Q MM LYK EK+NP+GGCFP+LIQMPIF ALY++L+ SVELRQAP+ WI D
 Sbjct: 414 GEDRQKFQQAAMMELYKKEKINPMGGCFPILIQMPIFFALYWVLVESVELRQAPWLWGIQD 473

Query: 458 LSAQDPYYILPILMGVTMFFIQKMSPTTV-TDPMQKIMTFMPVIFTVFFLWFPGLVLY 516
 L+ +DPY+ILP+L V M+ QK++PT DP+ K+M MP+IF V + PSGL LY
 Sbjct: 474 LTTRDPYFILPLNIVIMWATQKLTPTPAGMDPIAGKMMQVMPLIFGVMMFAFVPSGLALY 533

Query: 517 YIVSNLVTIIQQQLIYR 533
 ++++ + ++ Q + R
 Sbjct: 534 WVINGGLNLLIQWWMIR 550

>ref|ZP_00038120.1| COG0706: Preprotein translocase subunit YidC [Xylella fastidiosa
 Dixon]
 Length = 565

Score = 327 bits (838), Expect = 2e-88

Identities = 205/571 (35%), Positives = 314/571 (54%), Gaps = 30/571 (5%)

Query: 1 MDSQRNLLVIALLFVSFMIWQAWEQDKNPQPPQAQQTQTTTTA-----AGSAA 48
 M+ R LL+ + L V+ ++W W ++KN + + AG+
 Sbjct: 1 MNQTRVLLIFSWLTVATLLWMDWGNKKNETLEISASHNLGVDSHLELEHAVPQINAGAVP 60

Query: 49 -----DQGVSPASGQGLISVKTVDLDTINTRGGDVEQALLPAYPKELN-STQPFQLLETS 103
 Q + A+ + +I+V TDVL L ++ G + A L +P+ + +P +LL
 Sbjct: 61 VQKDSQLIAAAPKVPVINVTDDVLQLKLD--GFSILAADLLRFPQSKDRGAKPIKLLTDD 118

Query: 104 PQFIYQAQSGLTGRDGPDPNPANGPRPLYNVEKDAYVLAEGQNELQVPMTYTDAAGNTFTK 163
 P + Y A + G + P N L + Y LA Q+ L VP + T A G + +
 Sbjct: 119 PNYYPYSATTGWVSQSNPVP-NLSTFLPEQSGVSYKLANDQDRLVVPFVWTAANGVSIRR 177

Query: 164 TFLVKRGDYAVNVNYNVQNAGEKPLEISSFGQLKQSITLPPHLDTGSSNFALHTFRGAAY 223
 TF +RG YA+ + ++N+GE P F +L + + +P L+ +N +F GA +
 Sbjct: 178 TFTFERGRYAILIRDEIRNSGETPWNAYVFRKLSR-VPIPNILNRAMTNPDSFSFNGAVW 236

Query: 224 STPDEKYEKYKFDTIADNENLNISSEKGGWVAMLQQYFATAWIPHNDGTNNFYTANLGNGI 283
 + YE+ F ++ LN GGW+A+LQ +F TAWIP D + + A NG
 Sbjct: 237 YSEKGGYERRAFKDYMNDDGGLNREIGGGWIALLOHHFFTAWIPQKDQASLYLLAQ--NGS 294

Query: 284 AAIGYKSQPV-LVPGQTGAMNSTLWVGPEIQDKMAAV-APHLDLTVDYG---WLWFISQ 338
 I P V PGQ+ + LWVGP++ +++ LD VDY + I Q
 Sbjct: 295 RDIAELRGPAFTVAPGQSTMTEARLWVGPKLVEQITKEHVKGGLDRVVDYSRFQLMALIGQ 354

Query: 339 PLFKLLKWIHSFVGNWGFSSIIITFIVRGIMYPLTKAQYTSMAKMRMLQPKIQAMRERLG 398
 LF +L ++S + NWG++I+ + ++R MYPL+ AQY S AKMR QP++Q ++ER G
 Sbjct: 355 GLFWILSHLNSLLHNWGWAIWGLVLLRIAMYPLSAAQYKSAKMRKFQPRQLQKERYG 414

Query: 399 DDKQRISQEMMALYKAEKVNPLGGCFPLLIQMPIFLALYYMLMGSVELRQAPFALWIHDL 458
 +D+Q+ Q MM LYK EK+NP+GGCFP+LIQMPIF ALY++L+ SVELRQAP+ WI DL
 Sbjct: 415 EDRQKFQQAAMELYKKEKINPMGGCFPILIQMPIFFALYWVLVESVELRQAPWLGIQDL 474

Query: 459 SAQDPYYILPILMGVTMFFIQKMSPTTV-TDPMQKIMTFMPVIFTVFFLWFPGLVLYY 517
 + +DPY+ILP+L V M+ QK++PT DP+ K+M MP+IF V + PSGL LY+
 Sbjct: 475 TTRDPYFILPLLIVIMWATQKLTPTAGMDPIAGKMMQVMPLIFGVMAFVPSGLALYW 534

Query: 518 IVS-NLVTIIQQQLIYRGLEKRGHSREKKK 547
 +++ L +IQ +I++ + SRE K
 Sbjct: 535 VINGGLNLLIQWWMIHQYADF SRKRSRENIK 565

>ref|NP_954506.1| membrane protein, putative [Geobacter sulfurreducens PCA]
 Length = 531

Score = 293 bits (749), Expect = 3e-78

Identities = 193/555 (34%), Positives = 291/555 (52%), Gaps = 55/555 (9%)

Query: 4 QRNLLVIALLFVSFMIWQAW---EQDKNPQPQAQQT-TQTTTTAAGSAADQGV PASGQ GK 59
 +R L+ + L + F + A + P+P A T +Q + VPA Q
 Sbjct: 3 KRALIAVLSILFFYGYTALFSPPPKETPKPVATATQSQPAQQVTAAPVPVAVPAQPQPA 62

Query: 60 L-----ISVKTDVLDLTINTRGGDVEQALLPAY-----PKELNSTQPFQLLETSPQFIYQA 110
 + +SV T +T +T+GG +++ L Y P N T
 Sbjct: 63 VAARDVSVDTPAYSVTFTSTQGGSIKRLDLKRYHETAGPGGKNVT----- 106

Query: 111 QSGLTGRDGPDPNPANGPR-PLYNVEK-----DAYVLAEGQNELQVPMTYTDAAGNTF 161
 L D P N G R P + +++ DA + G+ + Q+ T+ AG T
 Sbjct: 107 ---LVSEDNPSNYTIGLRAPGFGLDQNAVFPVPSADALTVGPGGKK-QLSFTWVSPAGVTV 162

Query: 162 TKTFVLKRGDYAVNVNYNVNQAGEKPLEISSFGQLKQSITLPPHLDTGSSNFALHTFRGA 221
 TKT+ Y + + Y V N+G +SS Q Q+ L P + S F TF G
 Sbjct: 163 TKTYNFGSDGYGLEIQYQVTNSGSA--RVSSPVQTVQTYPLVPKVK--ESRF--ETF-GP 215

Query: 222 AYSTPDEKYEKYKFDTIADNEN-LNISSKGGWVAMLQQYFATAWI PHNDGTNNFYTANLG 280
 A D+ +E D + D E+ + W +YF +A + H
 Sbjct: 216 ATFAQDKLFE----DKVKDLESGAKTHAAPLWSGFADKYFLSAVLAHEGSMMAATIRKTA 271

Query: 281 NGIAAIGYKSQPV-LVPGQTGAMNSTLWVGPEIQDKMAAVAPHLDLTVDYGWLWFISQPL 340
 +G S + + PG+ A+ L+ GP+ D + A L+ ++ GW +++PL
 Sbjct: 272 SGYLENTISSPELSLNPGEGRALTYRLFFGPKDIDVLKAQGNSLERAINLGFAMLA KPL 331

Query: 341 FKLLKWIHSFVGNWGFSSIIITFIVRGIMYPLTKAQYTSMAKMRMLQPKIQAMRERLGDD 400
 LK+ H++ GN+G +IIIIIT I++ I YPLT + Y SM +M+ LQPK+Q +RE+ +D
 Sbjct: 332 LHSLKFFHNYTGNYGIAIIIIITVIIKVFYPLTHSSYKSMKEMQKLQPKMQQLREKYKND 391

Query: 401 KQRISQEMMALYKAEKVNPLGGCFPLLIQMPIFLALYYMLMGSVELRQAPFALWIHDL SA 460
 ++ +++ MM LY+ KVN+GGC P+L+Q+P+F ALY LM S+ELR APF LWI DL+A
 Sbjct: 392 REAMNRAMMELYQTHKVNPGGCLPMLVQIPVFFALYKALMFSIELRHAPFMLWITDLAA 451

Query: 461 QDPYYILPILMGVTMFFIQKMSPTTVTDPMQOKIMTFMPVIFTVFFLWFPSGLVLYYIVS 520
 +DPYY+ PI+MGVTM QKM+P+ + DP+QOK+M +PV+FT FL FPSGLVLY++V+
 Sbjct: 452 KDPYYVTPIIMGVTMVIQOKMTPSQM-DPVQOKMMMALPVVFTFMFLNFPSTGLVLYWLVN 510

Query: 521 NLVTIIQQQLIYRGL 535
 N++TIIQQ I R +
 Sbjct: 511 NVLTIIQQYYINRSI 525

>ref|ZP_00301338.1| COG0706: Preprotein translocase subunit YidC [Geobacter
 metallireducens GS-15]
 Length = 531

Score = 283 bits (725), Expect = 2e-75
 Identities = 171/519 (32%), Positives = 274/519 (52%), Gaps = 31/519 (5%)

Query: 29 PQPQAQQTQTOTTTTAAGSAADQGVPA-----SGQGKLISVKTDVLDLTINTRGGDV 79
 P P AQQ + A A+ VPA Q K I+V+T +T+GG +
 Sbjct: 26 PAPSAAQAVTGSQPGAPQASVAAPAPSPVPAAAVKAQQKEIAVETPDYTAVFSTQGGSL 85

Query: 80 EQALLPAYPKELNSTQPFQLL--ETSPQ-FIYQAQSGLTGRDGPDPNPANGPRPLYNVEKD 136
 + +L Y + + T L E P + ++ G D P L+ D
 Sbjct: 86 TRLVLLKKYRETADLTGKHVTLVDERDPSAYTLSTRAAGIGLD-----PSALFVSSAD 137

Query: 137 AYVLAEGQNELQVPMTYTDAGNTFTKTFVLKRGDYAVNVNYNVQNAGEKPLEISSFGQL 196
 + + G+ + ++ T+ AG T K + + G+Y +++ Y N+G + G
 Sbjct: 138 SLTVEAGEEKKELAFWISPAWTVRKYITFQGGNYGIDMVYQTANSQT-----ARVGAA 192

Query: 197 KQSITLPPHLDTGSSNFALHTFRGAAYSTPDEKEYEKYKFDTIADNENLNISCKGGWVAML 256
 Q++ P + + L TF ++ EK K D + ++ + W
 Sbjct: 193 FQTVMTYPAVPRVKES-RLETFGPVTFAQDKLTEEKVK-DLVGQGKSYSAPL---WSGFA 247

Query: 257 QQYFATAWIPHNDGTNNFYTANLNGIAAIGYKSQPVLVQPGQTGAMNSTLWVGPEIQDK 316
 +YF +A + + G+ + + PG++ ++ L+ GP+ D
 Sbjct: 248 DKYFLSAVVGQGGSIATAAVRSTPRGMLDITAPETSLNPGESKSVAYRLYFGPKDLDI 307

Query: 317 MAAVAPHLDLTVDYGWLWFIQPLFKLLKWIHSFVGNWGFSSIIITFIVRGIMYPLTKAQ 376
 + A L+ +D GW +++PL LK+ + +V N+G +IIIT I++ I YPLT +
 Sbjct: 308 LKAQGNSLERAIDLGFAMLAQLLHSLKFFYKYVHNYGIAIIITVILKIIFYPLTHSS 367

Query: 377 YTSMAKMRMLQPKIQAMRERLGDDKQRISQEMMALYKAQKVNPLGGCFPLLIQMPIFLAL 436
 Y SM +M+ LQPK+Q +RE+ +D+ +++ +M LY+ KVN+GGC P+L+Q+P+F AL
 Sbjct: 368 YKSMKQMQLQPKMQEVREKYKNDRDAMNKAIMELYQTHKVNPGGCLPMLVQIPVFFAL 427

Query: 437 YYMLMGVELRQAPFALWIHDLAQDPYYILPILMGVTMFFIQKMSPTTVTDPMQOKIMT 496
 Y LM S+ELR APF LWI DL+ +DPYY+ PI+MG+TM QKM+P+ + DPMQOK+M
 Sbjct: 428 YKALMFSIELRHAFMLWIDLAGKDPYYVTPIIMGITMVIQOKMTPSQM-DPMQOKMMM 486

Query: 497 FMPVIFTVFFLWFPSGLVLYYIVSNLVTIIQQQLIYRGL 535
 +PV+FT FL FPSGLVLY++V+N++TIIQQ I + +
 Sbjct: 487 ALPVVFTFMFLNFPSTGLVLYWLVNNVLTIIQQSYINKSI 525

>ref|ZP_00288574.1| COG0706: Preprotein translocase subunit YidC [Magnetococcus sp.
 MC-1]
 Length = 556

Score = 271 bits (693), Expect = 1e-71

Identities = 178/565 (31%), Positives = 283/565 (50%), Gaps = 47/565 (8%)

Query: 4 QRNLLVIALLFV---SFMWQAW-----EQDKNPQQAQQTQTTTTAA----- 44
 +R L I L FV +F + AW EQ ++ + A +T A

Sbjct: 3 RRTLTAVLSFVLLTAFQFYMAWKYPPAELTGEQVQSGESSAPAPLASTAPVADALPPP 62

Query: 45 -----GSAADQGVPA-----SGQGKLISVKTDVLDLTINTRGGDVEQALLPAYPKELNSTQP 96
 GSA Q + + L+ K D+++ ++ +GG + + L +P

Sbjct: 63 EGMAGSAPQQAQMSQPLINTDAKSLHFKNDLVEGSLSLQGGRLVGMDFLQHTDVLGG-KP 121

Query: 97 FQLETSPOFIYQAQSGLTGRDGPDPNPANGPRPLYNVEKDAYVLAEGQNELQVPMTYTDA 156
 + S + +SG G A P N + Q + + + +

Sbjct: 122 ISFMGISQVESFYQESGFLPVAGSAIKA----PDANTQWQLIGKESLQGAGEFKLVWDNG 177

Query: 157 AGNTFTKTFVLKRGDYAVNVNINVQNAGEKPLEISSFGQLKQSITLPPHLDTGSSNFALH 216
 G F K F +G Y V + N L + + Q K+ + S A+

Sbjct: 178 EGIVFEKLFSAQGSYLFKVEDRLINNSAAALGVYHYSQFKRIPVI-----NSQSMLAMS 232

Query: 217 TFRGAAYSTPDEKEYEKYKFDTIADNENLNISCKGGWVAMLQQYFATAWI-----PHNDGT 271
 F+G E+Y+ D A ++L GGW +YF A + P

Sbjct: 233 DFQGPMAVYNGERYQHSYEDLTA--QDLREKGGHGGWTGFSKYFLAAMVAKPLPPEAQPR 290

Query: 272 NNFYTANLGNIAAIGYKSQPVLVQPGQTGAMNSTLWVGPEIQDKMAAVAPHLDTVDYG 331
 ++ + N +G V++ GQ+ A++ L++GP+ + L+ ++DYG

Sbjct: 291 RYYFDYDRPN--YRVGMVENSVIIPAGQSLAVDYDLFIGPKEISTLERSNLSLERSIDYG 348

Query: 332 WLWFISQPLFKLLKWIHSFVGNWGFSSIIITFIVRGIMYPLTKAQYTSMAKMRMLQPKIQ 391
 W F+++PL K+L + +S V N+G +II++T ++ + +PL Y SM M+ LQPKI+

Sbjct: 349 WFHFLAEPLVKVLNFFNSVHNYGVAILLLTLAIKLLFFPLANKSYRSMNAMKKLQPKIE 408

Query: 392 AMRERLGDDKQRISQEMMALYKAQKVNPLGGCFPLLIQMPIFLALYMLMGSVELRQAPF 451
 +++ G D+ ++++ MM LY+ KVNPLGGC P+L+Q+P+F ALY +L SVE+R APF

Sbjct: 409 ELKKLHGSDRNKMNEAMMKLYQTHKVNPLGGCLPILVQIPVFFALYKVLFLSVEMRHAPF 468

Query: 452 ALWIHDLQAQDPYYILPILMGVTMFFIQKMSPTTVTDPMQKIMTFMPVIFTVFFLWFPS 511
 LWI DLSA DP+Y+LP+LMG +MF K++PT +DPMQ KIM F+PVIFTV FL FPS

Sbjct: 469 MLWIPDLSAMDPFYVLPPLMGSGMFLQSKLNPTP--SDPMQAKIMMFLPVIFTVMFLSFPS 527

Query: 512 GLVLYYIVSNLVTIIQQQLIYRGLE 536
 GLVLY++V+N+++I QQ I + +E

Sbjct: 528 GLVLYWLVNNVLSISQQYYIMKKME 552

>ref|NP_700186.1| inner-membrane protein, 60 kDa [Brucella suis 1330]
 Length = 610

Score = 269 bits (688), Expect = 4e-71

Identities = 185/602 (30%), Positives = 298/602 (49%), Gaps = 86/602 (14%)

Query: 1 MDSQRNLLV-IALLFVSFMIWQAW-----EQDK--NPQQAQQTQTTTTAAAGSA 47
 M+++RN + IAL + +WQ + EQ + Q QAQQ Q ++ +

Sbjct: 1 MENKRNFFITIALSILILALWQVLYLGPKTEAQREQARIEEQRQAQQAQNRQASSSTG 60

Query: 48 ADQGVFPAS-----GQGKL-----ISVKTDVLDLTINTRGGDVEQALL 84
 +PA+ GQG I + T L +IN G ++ L

Sbjct: 61 DTPQMPANPDSIPGQGDTKAAGAPLTRDAAIAQSPRIEIDTPSLRGSINLTGARLDDLYL 120

Query: 85 PAYPKELNSTQP-FQLETSPOFIYQAQSGLTGRDGPDPNPANGPRPLYNVEKDAYVLA 142

```

      Y + ++   P +LL S + Y + G TG D      GP ++ VE
Sbjct: 121 KKYHETVSDKSPEIELLAPSSLKQGYFVELGFTGNDAT-GAVPGPNTVWVVE----- 171

Query: 143 GQNELQ----VPMTYTDAGNTFTKTFVLKRGDYAVNVNYNVQNAGEKPLEISSFGQLKQ 198
      G N+L      V +TYT+      TF +      +      Y V+ + N G + ++S+G++ +
Sbjct: 172 GNNKLTPSTPVTLTYTNDKNLTFKRVISVDDA-YMFTVDDTIINNGGSTVSLASYGRVTR 230

Query: 199 SITLPPHLDTGSSNFALHTFRGAAYSTPDEKEYEKYKFDTIADNENLNISSEK-GGWVAMLQ 257
      P H      S+ + LH G      + ++ K+ I DN++++      GGWV +
Sbjct: 231 -FNQPEH---ASATYVLH--EGLIGVMGQDGLQEIKYAKIKDNKDISFKDVIGGWGITD 284

Query: 258 QYFATAWIPHNDG--TNNFYTANLGNIAAIGYKSPVLVQPGQTGAMNSTLWVGPEIQD 315
      +Y+A IP D T F      S P+ V PGQ+ + + ++ G ++ +
Sbjct: 285 KYWAATLIPPQDEKFTGRFSHFTNDRPRYQSDLLSAPLTVAPGQSQKIQNRVFAKAVVN 344

Query: 316 KMAAVAP-----HLDLTVDYGWLWFISQPLFKLLKWIHSFVGNWGFSSIIITFIVRGIMY 370
      +      DL +D+GW +FI++P+F L+ WI+ F GN+G +I+++T +++ + +
Sbjct: 345 TIQNYETKYHIKQFDLLIDWGWIFYFITKPMFYLIDWIYKFTGNFGVAILVVTVLKALFF 404

Query: 371 PLTKAQYTSMAKMRMLQPKIQAMRERLGDDKQRISEMMALYKAEKVNPLGGCFPLLIQM 430
      PL Y SMA+M+++QPK+ +RE+ DDK + Q MM LYK EK+NPL GC+P+L+Q+
Sbjct: 405 PLANKSYKSMARMKLMQPKMTEIREKYADDKMKQQQAMMELYKREKINPLAGCWPVLVQI 464

Query: 431 PIFLALYYMLMGSVELRQAPFALWIHDLQAQDPYYIL-----PILM 471
      P+F ALY +L ++E+R APF WI DL+A DP I      PI+M
Sbjct: 465 PVFFALYKVLVYVTIEMRHAPFFGWIQDLAAPDPTSIFNLFGLLPYTVPHFLMIGVWPIIM 524

Query: 472 GVTMFFIQKMSPTTVDTPMQQKIMTFMPVIFTVFFLWFPGLVLYYIVSNLVTTIIQQQLI 531
      G+TMF +M+PT DP Q I T+MP+IFT      FP+GLV+Y+ +N ++IIQQ +I
Sbjct: 525 GITMFLQMRMNPTP-PDPTQAAIFTWMPIIFTFMLASFAGLVIYWAWNNTLSIIQQSVI 583

Query: 532 YR 533
      +
Sbjct: 584 MK 585

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>ref|NP_384550.1| PUTATIVE INNER-MEMBRANE TRANSMEMBRANE PROTEIN [Sinorhizobium meliloti 1021]
Length = 595

Score = 266 bits (679), Expect = 4e-70

Identities = 180/590 (30%), Positives = 300/590 (50%), Gaps = 77/590 (13%)

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Query: 1 MDSQRNLLV-IALLFVSFMIWQAW-----EQDKNPQPQAQQTQTTTTAAAGSAADQG-- 51
      M++ RN V IAL + + WQ +      E+D+ QAQQ QT      A G
Sbjct: 2 MENNRNYFVAIALSVLILIAWQFFVYSPKMEKDRIAAEQQAQQAQQTQQQPGAQPAAPGQA 61

Query: 52 -----VPASGQGK-----LISVKTDVLDLTINTRGGDVEQALLPAYPKELNSTQP-- 96
      +P++G+ +      +++ T L +IN G + L Y + ++ P
Sbjct: 62 LPGGAIPSAAGESRDQAIGKSARVAIDTPALSGSINLTGARFDDLKLGKGYRETVPKSPVI 121

Query: 97 --FQLLETSPQFIYQAQSGLTGRDGPDPNPANGPRPLYNVEKDAYVLAEGQN---ELQVPM 151
      F ET+ + +      G G D + P P      + + L+ G      V +
Sbjct: 122 TLFSPAETADGYFTEI-----GYIGSDATGSVPGP-----QTTWTLSGGDKLTPSTPVTL 171

Query: 152 TYTDAAGNTFTKTFVLKRGDYAVNVNYNVQNAGEKPLEISSFGQLKQSITLPPHLDTGSS 211
      +YT+ G TF +T +      Y V +++N P+ +SS+G++ +      + T S
Sbjct: 172 SYTNDKGITFARTISVD-DRYMFQVVDISIKNETAAPVSLSSYGRVTRF-----NKPTTPS 225

```

Query: 212 NFALHT-FRGAAYSTPDEKEYEKYKFDTIADNENLNIS-SKGGWVAMLQQYFATAWIPHND 269
 + LH F G A + ++ + + D+E + S GGW+ + +Y+A +P
 Sbjct: 226 IYVLHEGFVGVA---GEHGLQEVGYSKVEDDEPVEPGKSTGGWLGITDKYWAATIVPPQA 282

Query: 270 GTNNFYTANLNGIAAI--GYKSQPVLVQPGQTGAMNSTLWVG----PEIQD-KMAAVAP 322
 + ++ +G YKS V V PGQ+ + + ++ G P + + ++A P
 Sbjct: 283 TPFDIRFSHFADGRPRYQSDYKSDAVTVAPGQSVELKNLVFAGAKEVPVVDNIEVAYSIP 342

Query: 323 HLDLTVDYGWLWFISQPLFKLLKWIHSFVGNWGFSSIIITFIVRGIMYPLTKAQYTSMAK 382
 + D +D+GW +FI++P+FK++ + GN+G +I+I T +V+ I +PL QY SMA
 Sbjct: 343 NFDKLIDWGWFFYFITKPMFKMMDFFRFLGNGFIAILITTIVVKLIFFPLANKQYASMAN 402

Query: 383 MRMLQPKIQAMRERLGDDKQRISQEMMALYKAEKVNPLGGCFPLLIQMPIFLALYYMLMG 442
 M+ +QPK++ +++++ GDD+ + Q MM LYK EK+NPL GC+P+LIQ+P+F ALY ++
 Sbjct: 403 MKKVQPKMEELKKKFGDDRMGLQQAMMQLYKEEKINPLAGCWPILIQIPVFFALYKVIYV 462

Query: 443 SVELRQAPFALWIHDLQAQDPYYIL-----PILMGVTMFFIQKMSP 483
 ++E+R APF WI DLSA DP I+ PI+MGVTMF +M+P
 Sbjct: 463 TIEMRHAPFFGWIQDLSAPDPTTIINLFLGLLPFEGPAFLHLGIWPIIMGVTMFLQMRMNP 522

Query: 484 TTVTDPMQQKIMTFMPVIFTVFFLWFPGLVLYYIVSNLVTIIQQQLIYR 533
 T DP Q + T+MPV+FT FP+GLV+Y+ +N ++I+QQ +I +
 Sbjct: 523 TP-PDPTQAMLFTWMPVVFTFMLASFPAGLVIYWAWNNTLSILQQGIIMK 571

>ref|NP_541252.1| 60 kDa inner membrane protein YidC [Brucella melitensis 16M]
 Length = 588

Score = 264 bits (674), Expect = 2e-69

Identities = 170/529 (32%), Positives = 272/529 (51%), Gaps = 51/529 (9%)

Query: 38 QTTTTAAGSAADQGV PASGQGLISVKT DVLDTINTRGGDVEQALLPAYPKELNSTQP- 96
 Q T AAG+ + A Q I + T L +IN G ++ L Y + ++ P
 Sbjct: 53 QGDTKAAGAPLTRDA-AIAQSPRIEIDTPSLRGSINLTGARLDDLYLKHYETVSDKSPE 111

Query: 97 FQLELTSP-QFIYQAQSGLTGRDGPDPNPANGPRPLYNVEKDAYVLAEGQNELQ----VPM 151
 +LL S + Y + G TG D GP ++ VE G N+L V +
 Sbjct: 112 IELLAPSSLKQGYFVELGFTGN DAT-GAVPGPNTVWVVE-----GNNKLTPSTPVTL 162

Query: 152 TYTDAAGNTFTKTFVLKRGDYAVNVNYNVNQAGEKPLEISSFGQLKQSITLPPHLDTGSS 211
 TYT+ TF + + Y V+ + N G + ++S+G++ + P H S+
 Sbjct: 163 TYTNDKNLTFKRVISVDDA-YMFTVDDTIINNGGSTVSLASYGRVTR-FNQPEH---ASA 217

Query: 212 NFALHTFRGAAYSTPDEKEYEKYKFDTIADNENLNIS-SKGGWVAMLQQYFATAWIPHNDG 270
 + LH G + ++ K+ I DN++++ GGWV + +Y+A IP D
 Sbjct: 218 TYVLH--EGLIGVMGQDGLQEIKYAKIEDNKDISFKDVIGGWVGITDKYWAATLIPPQDE 275

Query: 271 --TNNFYTANLNGIAAIGYKSQPVLVQPGQTGAMNSTLWVGPEIQDKMAAVAP----H 323
 T F S P+ V PGQ+ + + ++ G ++ + +
 Sbjct: 276 KFTGRFSHFTNDRPRYQSDLLSAPLTVAPGQSQKIQRNVFAGAKVVNTIQNYETKYHIKQ 335

Query: 324 LDLTVDYGWLWFISQPLFKLLKWIHSFVGNWGFSSIIITFIVRGIMYPLTKAQYTSMAK 383
 DL +D+GW +FI++P+F L+ WI+ F GN+G +I+++T +++ + +PL Y SMA+M
 Sbjct: 336 FDLLIDWGWFFYFITKPMFYLDWIYKFTGNFVGAILVTVLLKALFFPLANKSYKSMARM 395

Query: 384 RMLQPKIQAMRERLGDDKQRISQEMMALYKAEKVNPLGGCFPLLIQMPIFLALYYMLMGS 443
 +++QPK+ +RE+ DDK + Q MM LYK EK+NPL GC+P+L+Q+P+F ALY +L +
 Sbjct: 396 KLMQPKMTEIREKYADDKMQQAMMELYKREKINPLAGCWPVLVQIPVFFALYKVLVYT 455

Query: 444 VELRQAPFALWIHDLQAQDPYYIL-----PILMGVTMFFIQKMSPT 484
 +E+R APF WI DL+A DP I PI+MG+ MF +M+PT
 Sbjct: 456 IEMRHAPFFGWIQDLAAPDPTSIFNLFGLLPYTPHFLMIGVWPIIMGIIMFLQMRMNPT 515
 Query: 485 TVTDPMQKIMTFMPVIFTVFFLWFPSGLVLYIVSNLVTIIQQQLIYR 533
 DP Q I T+MP+IFT FP+GLV+Y+ +N ++IIQQ +I +
 Sbjct: 516 P-PDPTQAAIFTWMPPIIFTFMLASFPAGLVIYWANNNTLSIIQQSVIMK 563

>ref|ZP_00055732.1| COG0706: Preprotein translocase subunit YidC [Magnetospirillum
 magnetotacticum MS-1]
 Length = 578

Score = 263 bits (673), Expect = 2e-69
 Identities = 181/598 (30%), Positives = 294/598 (49%), Gaps = 80/598 (13%)

Query: 1 MDSQRNLLVIALLFVSFMI-WQ-----AWEQDKNPQQAQQTQTOTTTTAAGS 46
 M+ QRNL V + V+ +I WQ A +Q + A + TA+
 Sbjct: 1 MNDQRNLFVAIAISVAILIGWQYFFPTAKPPVEQAAQQQAQAEVKASAPANVPSPATASSP 60
 Query: 47 AADQGVPA-----GQGLISVKTDVLDLTINTRGGDVEQALLPAYPKELNST 94
 A G PA+ G+ + I+++T + +I G ++ L Y +E +
 Sbjct: 61 AQVPGTPAAAAQTGASRNEALGKSRRIAIQTSPMHGSIALTGARIDITLVKY-RETPAA 119
 Query: 95 QPFQLLETSPQFI---YQAQSGLTGRDGPDPNPANGPRPLYNVEKDAYVLAEGQNELQ--- 148
 ++ SP Y A+ G D + GP ++ A+G L
 Sbjct: 120 DSAEIDLMSPAESPEPYWAEFGWVATDA-NVKVPGPESVWQ-----AQGTGPLTQAS 170
 Query: 149 -VPMTYTDAAGNTFTKTFVLKRGDYAVNVNYNVQNAGEKPLEISSFGQLKQSITLPPHLD 207
 V +T+ + G F +T+ + +Y V V+N G K + + L ++ T PH+
 Sbjct: 171 PVVLTWDNGEGLRFVRTYTVDE-NYMFVGTQRVENYGTAAASLHPYALLARTGT--PHV- 226
 Query: 208 TGSSNFALHTFRGAAYSTPDEKYEKYKFDTIADNENLNISSKGGWVAMLQQYFATAWIP- 266
 + + LH + D ++ K+D + + + GGW + +Y+ TA +P
 Sbjct: 227 --AGMYILHEGPLGVF---DGTLEKEMKYDDLKKEGSARYKTTGGWAGITDKYWLTAALVPP 281
 Query: 267 -HNDGTNNFYTANLGNIA-AIGYKSQPVLVQPGQTGAMNSTLWVGPEIQDKMAAVAP-- 322
 + T F LGN + Y + +++ G+T L+ G + +
 Sbjct: 282 AKTEITGRFVHQRLGNADRYQVDYLAPARVIEAGKTEEAGFHLFTGAKQVSLLDGYGEKF 341
 Query: 323 ---HLDLTVDYGWLWFISQPLFKLLKWIHSFVGNWGFSSIIITFIVRGIMYPLTKAQYTS 379
 DL +D+GW +F+++P F LL+ +HS +GN G +I+ +T I++ M+PL Y +
 Sbjct: 342 GIDRFDLAIDFGWYFYLTKPFFYLLQMLHSALGNMGLAILALTIVILKLAMFPLANKSYVA 401
 Query: 380 MAKMRMLQPKIQAMRERLGDDKQRISQEMMALYKAQKVNPLGGCFPLLIQMPIFLALYYM 439
 M KM+ LQPK+Q ++ R DDK R+ QEMMALYKAQKVN+ GC P+++Q+P+F ALY +
 Sbjct: 402 MGKMKKLQPKVQELQARYADDKMRLQEMMALYKAQKVN+VSGCLPIMVQIPVFFALYKV 461
 Query: 440 LMGSVELRQAPFALWIHDLQAQDPYYIL-----PILMGVTMFFIQK 480
 L ++E+R APF WI DLSAQDP I P++MG+TM+ QK
 Sbjct: 462 LFTVTIEMRHAPFYGWISDLSAQDPTNIFTLFLGLIPWTPPHIMHLGVWPLIMGITMYLQOK 521
 Query: 481 MSPTTVTDPMQKIMTFMPVIFTVFFLWFPSGLVLYIVSNLVTIIQQQLIYRGLEKR 538
 ++P TDP+Q K+M F+P+IFT F SGLV+Y+ SN ++I+QQ +I + E++
 Sbjct: 522 LNPQP-TDPVQAKMMQFLPLIFTFLLANFASGLVIYWAWSNTLSILQQWVIMKRAEEK 578

>ref|YP_010298.1| inner membrane protein, 60 kDa [Desulfovibrio vulgaris subsp.

vulgaris str. Hildenborough]
Length = 534

Score = 256 bits (654), Expect = 4e-67
Identities = 170/558 (30%), Positives = 279/558 (50%), Gaps = 51/558 (9%)

Query: 1 MDSQRNLLVIALLFVSMIWAWEQDKNPQQAQQTQTTTTAAG-----SAADQGV 53
M+++R ++ + L F+ + W + P++ T+ T A+ SA + P
Sbjct: 1 MENKRAIIAVVLSFIVLVGWGYLSEYMGWTPKSVPAEQKTAASAPAPSVVTSAPAVTP 60

Query: 54 ASG----QGKLISVKTDVLDLTINTRGGDVEQALLPAYPKELN-STQPFQLLETSPQFIY 108
A G ++V T + +++ GG + Q +L Y ++ P L+E+S I
Sbjct: 61 APAFSPSTGHEVTVTTPPLYKAVLHSGGGVLRQFMLSRYHMGIDRDAAPVNLISSA--IR 118

Query: 109 QAQSGLTGRDGPDPNANGPRPLYNVEKDAYV-----LAEGQNELQVPMTYTDAAGNTFTK 163
A GL NG +P +N + A+ LA+GQ + D G +
Sbjct: 119 VAPLGLL-----VNG-QPSWNTGQWAFEGGDLNLADGQTGTLRFVGSVD--GLRVVR 167

Query: 164 TFVLKRGDYAVNVNYNVQNAKEKPLEISSFGQLKQSITLPPHLDTGSSNFALHTFRGAAY 223
Y V ++ G+ P + G + +L P G S + L A
Sbjct: 168 ELEFHADSILVTEKLHLAPEGDAP-RTARVGFTLGTTSITP----GESQYNLTRVAFAD 222

Query: 224 STPDEKYEKYKFDTIADNENLNISKGGWVAMLQQYFATAWIPHNDGTNNFYTANLNGI 283
+ EK + + + I W ++ YF A P + T L G+
Sbjct: 223 GSFSEKSSTGDLE-----KGVLDIGSIDWAGVMSNYFLAAVAPKD--TRAVLKGKLEGGV 275

Query: 284 AAIGYKSQPVLVQPGQTGAMNSTLWVGPEIQDKMAAVAPHLDLTVDYGWLWFISQPLFKL 343
+ + +V PG + + W GP+ +D + A +L +D GW FI++PL L
Sbjct: 276 YRVAVERPDQMVNPGNSDVIVCNYWFGPKERDLLNAAPNNLGAIDLGWFGFIARPLVTL 335

Query: 344 LKWIHSFVGNWGFSSIIITFIVRGIMYPLTKAQYTSMAKMRMLQPKIQAMRERLGDDKQR 403
L + + +VGN+G +II++T +++ + +PL+ Y SM +M+ LQP + +RE+ DD+++
Sbjct: 336 LDDFYKYVGNYGTAIILLTILIKLVFWPLSHKSYKSMEQMKKLQPLAKVREKHADDREK 395

Query: 404 ISQEMMALYKAEKVNPLGGCFPLLIQMPIFLALYYMLMGVSVELRQAPF-----ALWI 455
+++EMM LYK KVNPGGC P+L+Q+P+F LY L+ ++ELR APF +W+
Sbjct: 396 MNEEMMRLYKTYKVNPAAGCLPMLVQIPVFFGLYQALLNAIELRHAPFIAHVPFTDIVWL 455

Query: 456 HDLSAQDPYYILPILMGVTMFFIQKMSPTTVDTPMQQKIMTFMPVIFTVFFLWFPSGLVL 515
DLSA+DP+Y+ P++MG TMF QK++P DP Q K+M FMPV+FT FL FPSGLV+
Sbjct: 456 ADLSAKDPFYVTPLVMGATMFLQQLTP-PAGDPTQAKVMMFMPVVFTFLFLNFPGLV 514

Query: 516 YYIVSNLVTIIQQQLIYR 533
Y++ +N+++I QQ I R
Sbjct: 515 YWLCNNVLSIAQQWILR 532

>ref|ZP_00321289.1| COG0706: Preprotein translocase subunit YidC [Haemophilus
influenzae 86-028NP]
Length = 221

Score = 255 bits (652), Expect = 6e-67
Identities = 118/159 (74%), Positives = 139/159 (87%)

Query: 386 LQPKIQAMRERLGDDKQRISQEMMALYKAEKVNPLGGCFPLLIQMPIFLALYYMLMGVSVE 445
+QPK+Q MRER GDD+QR+SQEMM LYK EKVNPLGGC P+L+QMPIF+ALY+ + +VE
Sbjct: 1 MQPKMQEMRERFGDDRQMSQEMMKLYKEEKVNPLGGCLPILLQMPIFIALYWTFLEAVE 60

Query: 446 LRQAPFALWIHDLAQDPYYILPILMGVTMFFIQKMSPTTVDTPMQQKIMTFMPVIFTVF 505

Sbjct: 61 LRAPFFGWIQDLAQDPYYILPILMG++MF +QKMSPT VTDP QOK+M FMP++ F
 Query: 506 FLWFPSGLVLYIYVSNLVTIIQQQLIYRGLEKRGHLSRE 544
 FLWFPSGLVLY++VSNL+TI QQQLIYRGLEK+GLHSR+
 Sbjct: 121 FLWFPSGLVLYWLVSNLITIAQQQLIYRGLEKKGLHSRK 159

>ref|NP_282110.1| putative membrane protein [Campylobacter jejuni subsp. jejuni NCTC
 11168]
 Length = 528

Score = 253 bits (646), Expect = 3e-66

Identities = 126/316 (39%), Positives = 193/316 (61%), Gaps = 13/316 (4%)

Query: 216 HTFRGAAYSTPDEKYEKYKFDTIADNENLNISKGGWVAMLQQYFATAWIPHNDGTNNFY 275
 +T GA E E YK + +E+ N + +Y+AT FY
 Sbjct: 211 YTVHGALVMDNKETIETIKDGDVEKDESAN---NVVMTSAFDRIYATF-----FY 257
 Query: 276 TANLGNIAAIGYKSQPVLVQPGQTGAMNSTLWVGPEIQDKMAAVAPHLDLTVDYGWLWF 335
 + +A +Q +V + ++G + + ++ P L+ V+YGW F
 Sbjct: 258 NFDKPLNVAISKDANQNPIVFAYSDFNEFKAGGYIGSKEHVILRSIDPRLEAVVEYGWFTF 317
 Query: 336 ISQPLFKLLKWIHSFVGNWGFSSIIITFIVRGIMYPLTKAQYTSMAKMRMLQPKIQAMRE 395
 I++P+F+ L ++H ++GNWG++I+++T IVR I++PLT SM K++ L PK++ +RE
 Sbjct: 318 IAKPMFEFLNHLHQYIGNWGWAIIVMTLIVRIILFPLTYKSMISMNKLKDLAPKMKDIRE 377
 Query: 396 RLGDQKQRIQEMMALYKAQKVNPLGGCFPLLIQMPIFLALYMLMGSLVELRQAPFALWI 455
 R D Q+++ MM LYK NP+ GC P+L+Q+PIF A+Y +L+ ++EL+ AP+A WI
 Sbjct: 378 RYKGDQKQMNMMHMELYKKHGANPMMSGCLPILLQIPIFFAIYRVLLNAIELKAAPWAFWI 437
 Query: 456 HDLSAQDPYYILPILMGVTFMFFIQKMSPTTVDTPMQQKIMTFMPVIFTVFFLWFPSGLVL 515
 HDLS DPY+ILPILMG TMF Q ++P T+ DPMQ KIM F+PVIFT FF+ FP+GL L
 Sbjct: 438 HDLSVMDPYFILPILMGATMFLQQLITPMTIQDPMQAKIMKFLPVIFTFFFITFPAGLTL 497
 Query: 516 YYIVSNLVTIIQQQLI 531
 Y+ V+NL +++QQ +I
 Sbjct: 498 YWFVNNLCSLVQQWVI 513

>ref|NP_531090.1| 60 kd inner-membrane protein [Agrobacterium tumefaciens str. C58]
 ref|NP_353415.1| AGR_C_674p [Agrobacterium tumefaciens str. C58]
 Length = 600

Score = 252 bits (643), Expect = 7e-66

Identities = 175/602 (29%), Positives = 296/602 (49%), Gaps = 96/602 (15%)

Query: 1 MDSQRNLLV-IALLFVSFMIWQAW-----EQDKNPQPQAQQTQTQTTT-----AAGSAA 48
 M+ RN + IAL V + WQ EQ + + Q QTT AA A
 Sbjct: 2 MEKNRNYFIAIALSVVIVLAWQFLYMNPRIEQQRRAEEARQAQQTQQQPAPGAAPGAT 61
 Query: 49 DQGVF-----ASGQGLISVKTDLVLDLTINTRGGDVEQALLPAYPKELNS 93
 +G P A + + +++ T+ + +IN G + L Y + ++
 Sbjct: 62 VEGAPPASSTQAAATATREEAIARTQRAVDITNAIAGSINLTGARFDDIRLKGHYETVDD 121
 Query: 94 TQP----FQLLETSPQFI----YQAQSGLTGRDGPDPNANGPRPLYNVEKDAYVLAEGQN 145
 + P F +T + Y A + G GP + LA G
 Sbjct: 122 SSPIITLFPADTKDGYFTELGYVAAQEVGGVPGPTT-----VWTLASGDK 167

Query: 146 ELQ---VPMTYTDAAGNTFTKTFVLKRGDYAVNVNYNVQNAGEKPLEISSFGQLKQSI-- 200
 + V +TYT++ G F++T + Y +++ V+N G+ + +++G++ ++
 Sbjct: 168 LTETTPVTLTYSNSKGVVFSRTVSIIDE-HYMLSIADKVENPGQAAISFATYGRVTRNNKP 226

Query: 201 TLPPHLDTGSSNFALHT-FRGAAYSTPDEKYEKYKFDTIADNENLNISSEKGGWVAMLQQY 259
 +PP F +H F G S D + K+ + + + GGW+ + +Y
 Sbjct: 227 VIPPV-----FVIHEGFLGV--SGKDGSLTEKKYKDVEEEPVTVAKATGGWLGITDKY 277

Query: 260 FATAWIPHNDGTNNF---YTANLNGIA-AIGYKSQPVLVQPGQTGAMNSTLWVGPE--- 312
 +A A +P T F Y+ GN + +KS + V+ GQ+ + S ++ G +
 Sbjct: 278 WAAAIVPPQ--TTPFETRYSHITGNQPSYQADFKSDSMTVEAGQSIELKSLVFAGAKEVP 335

Query: 313 IQDKMAAV--APHLDLTVDYGWLWFISQPLFKLLKWIHSFVGNWGFSSIIITFIVRGIMY 370
 + D+ P DL +D+GW +FI++P+FK++ + + GN+G +I++ T +V+ + +
 Sbjct: 336 LVDRYETEYSVPKFDLLIDWGWIFYFITKPMFKMMDFFFRYFGNFGVAILLTIVVKALFF 395

Query: 371 PLTKAQYTSMAKMRMLQPKIQAMRERLGDDKQRISQEMMALYKAKEKNPLGGCFPLLIQM 430
 PL QY SMA M+ +QPK++ ++ + GDD+ + Q MM LYK EK+NP+ GC+P+L+Q+
 Sbjct: 396 PLASKQYASMANMKRMQPKMEELKAKHGDDRMAMQAMQLYKEEKINPVAGCWPMLLQI 455

Query: 431 PIFLALYYMLMGSVELRQAPFALWIHDLQAQDPYYIL-----PILM 471
 P+F ALY ++ ++E+R APF WIHDLA DP + P++M
 Sbjct: 456 PVFFALYKVIYVTIEMRHAPFFGWIHDLAPDPTSLFNLFLGLLPYDVPFLMIGVWPLVM 515

Query: 472 GVTMFFIQKMSPTTVDTPMQQKIMTFMPVIFTVFFLWFPSGLVLYYIVSNLVTIIQQQLI 531
 G+TMF +M+PT DP Q I T+MP+IFT FP+GLV+Y+ +N ++I QQ LI
 Sbjct: 516 GITMFLQMRMNPTP-PDPTQAMIFTWMPLIFTFMLASFPAGLVIYWAWNNTLSISQQALI 574

Query: 532 YR 533
 +
 Sbjct: 575 MK 576

>ref|ZP_00339791.1| COG0706: Preprotein translocase subunit YidC [Rickettsia akari s
 Hartford]
 Length = 560

Score = 249 bits (636), Expect = 4e-65

Identities = 171/566 (30%), Positives = 280/566 (49%), Gaps = 56/566 (9%)

Query: 6 NLLVIALLFVSFMI-WQAW----EQDKNPQQAQQT-----QTTTAAAGSAADQGV PAS 55
 NL+ +L +S + WQ + EQ K Q A Q Q A D V
 Sbjct: 7 NLIAAIVLSLSIIFGWQYFVIKPEQKKQQQIAVQKAANLKKQQLKALVEPATDIVVQEE 66

Query: 56 GQGKLISVKTDLVDLTINTRGGDVEQALLPAYPKEL--NSTQPFQLLETSPQFIYQAQSG 113
 Q + I ++++ L +I+ +G + +L Y ++L NS+ T+ + Y A+ G
 Sbjct: 67 SQVQRIKIESESLTGSISLKLGRFDDLLIKKYQDLSKNSSDVVLFSPNTTEHSYFAEIG 126

Query: 114 LTGRDGPDPNPANGPRPLYNVEKDAYVLAEGQNELQVPMTYTDAAGNTFTKTFVLKRGDYA 173
 L N D +L+ E V + + + G F T + + +Y
 Sbjct: 127 LVSNLSSVKLPNNDTIW---SSDGEILSP---EKPVNLFWVNEDGVKFLVTITVDK-NYL 179

Query: 174 VNVNYNVQNAGEKPLEISSFGQLKQSITLPPHLDTGSSNFALHTFRGAAYSTPDEKYEKY 233
 + + N +K L I S+G + + T + A++ DE ++Y
 Sbjct: 180 FTIEQTIVNNSDKELPIQSYGLINRKYT-----AVEKAVNILHQGPICIDENLKEY 231

Query: 234 KFDTIADNENLNIS-SKGGWVAMLQQYFATAWIPH---NDGTNNFYTANLNGIAAIGYK 289
 +D I D ++ + SK W+ + +Y+ +A IP N +N Y G + +

Sbjct: 232 SYDDIKDKKSEKFAASKVDWIGITDKYWLSALIPDKSSNYSSNFNYAVKQGIEKYQVDFI 291

Query: 290 SQPVLVQPGQTGAMNSTLWVGPEIQDKMAAVAPHLDL-----TVDYGWLWFISQPLFKLL 344
S +++PG+ A+ S ++ G + D + D+ +D+GW + I++P+F +

Sbjct: 292 SPVQIIKPGENFAIKSRIFAGAKKVDLLDQYEKQYDIKLFDRIDFGWFYIITKPVFYAM 351

Query: 345 KWIHSFVGNWGFSSIIITFIVRGIMYPLTKAQYTSMAKMRMLQPKIQAMRERLGDDKQRI 404
+ + +VGN+G SI+I+T I++ +M+ L Y SM K++ LQP+I ++ DDK.R+

Sbjct: 352 NFFYGYVGNFVGSILIVTVIIKLLMFTLANKSYRSMKKIKNLQPEIDRIKNLYSDDKARL 411

Query: 405 SQEMMALYKAEKVNPLGGCFPLLIQMPIFLALYYMLMGVELRQAPFALWIHDLQAQDPY 464
+QE+MALYK EKVNP+ GC P+L+Q+P+F ++Y +L ++E+RQA F WI DLQA DP

Sbjct: 412 NQEIMALYKKEKVNVPVAGCLPILVQIPVFFSIYKVLVYVTIEMRQAQFYGWIKDLSAPDPT 471

Query: 465 YIL-----PILMGVTMFFIQKMSPTTVDPMQKIMTFMPVIFTVF 505
I PILM +TMF QKMSP DPMQ ++M FMP+IF

Sbjct: 472 TIFNLFGLLPFSPPSFLMIGAWPILMAITMFLQKMSPEP-ADPMQAQVMKFMPLIFLFM 530

Query: 506 FLWFPSGLVLYIIVSNLVTIIQQQLI 531
F FP GL++Y+ +N+++IIQQ I

Sbjct: 531 FSSFPGVLLIYWSWNNILSIIQQYYI 556

>ref|NP_105597.1| hypothetical protein mlr4812 [Mesorhizobium loti MAFF303099]
Length = 603

Score = 249 bits (635), Expect = 6e-65

Identities = 165/534 (30%), Positives = 274/534 (51%), Gaps = 70/534 (13%)

Query: 40 TTTAAGSAADQGVASGQGLISVKTDLVLDLTINTRGGDVEQALLPAYPKELNSTQPFQL 99
T T AG DQ + AS K + + T L+ +IN G ++ L Y + ++ P ++

Sbjct: 76 TVTVAGR--DQALAAS---KRVKIDTPSLEGSINLTGARLDDLKLKHYTETVDKNSP-EI 129

Query: 100 LETSPQFI---YQAQSGLTGRDGPDPNANGPRPLYNVEKDAYVLAEGQNELQVPMTYTDA 156
+PQ + Y A+ G G D G ++NV+ + + V +TYT+

Sbjct: 130 ELLNPQALPTGYFAEIGFVGND-KTGAVPGAETVWNVVDGNPTL----SPSTPVTLTYTND 184

Query: 157 AGNTFTKTFVLKRGDYAVNVNYNVQNAGEKPLEISSFGQLKQSITLPPHLDTGSSNFALH 216
G TF +TF + +Y V+ VQN+G + + ++G++ + +S + LH

Sbjct: 185 KGLTFKRTFSDV-ANYMFTVSDTVQNSGSSAVSLFNIGRVTRY-----DKPAVASTYVLH 238

Query: 217 TFRGAAYSTPDEKEYEKYKFDITIA-DNENLNISKGGWVAMLQQYFATAWIP----- 266
G T E +++K+ +I D + + GW+ + +Y+A +P

Sbjct: 239 --EGLIGFTGTEGLQEHKYASIEKDKYQPGKATDGWLGITDKYWAVTLVPTEKQPFQPR 296

Query: 267 ---HNDGTNNFYTANLGNIAAIGYKSQPVLVQPGQTGAMNSTLWVGPEIQDKMAAVAP- 322
DG + + + L + I V+ GQ+ + + ++ G + K+ A A

Sbjct: 297 YAFFEDGRHRYQSDFLTDAIN-----VEAGQSATVETEVFAGAKEVAKINAYAED 346

Query: 323 ----HLDLTVDYGWLWFISQPLFKLLKWIHSFVGNWGFSSIIITFIVRGIMYPLTKAQYT 378
DL +D+GW FI++P+F L+ ++ F+GN+G +I+ T IV+ + +PL Y

Sbjct: 347 RHIKRFDLLIDWGWFWHFITKPMFWLIDTLYKFLGNFGLAILATTVIVKALFFPLANKSYA 406

Query: 379 SMAKMRMLQPKIQAMRERLGDDKQRI SQEMMALYKAEKVNPLGGCFPLLIQMPIFLALYY 438
SMA M+ +QPK+ +RE+ DDK + Q MM LYK EK+NPL GC+P+ +Q+P+F +LY

Sbjct: 407 SMANMKKVQPKMLEIREKYADDKMKQQQAMMELYKTEKINPLAGCWPVALQIPVFFSFLYK 466

Query: 439 MLMGSVELRQAPFALWIHDLQAQDPYYIL-----PILMGVTMFFIQ 479
+L ++E+R APF WI DL+A DP + P++MGVTMF

Sbjct: 467 VLYITIEMRHAPFFGWIQDLAAPDPTSLFNLFGFLIPVTLPHMLMIGVWPLIMGVMTMFLQM 526

Query: 480 KMSPTTVTDPMQQKIMTFMPVIFTVFLLWFPSGLVLYYIVSNLVTIIQQQLIYR 533
+M+PT DP Q I T+MPVIFT FP+GLV+Y+ +N+++I+QQ +I +

Sbjct: 527 RMNPTP-PDPTQAAIFTWMPVIFTFMMAGFPAGLVIYAWNNMLSILQQGVIMK 579

>gb|EAA25857.1| 60 kD inner-membrane protein [Rickettsia sibirica 246]
ref|ZP_00142448.1| 60 kD inner-membrane protein [Rickettsia sibirica 246]
Length = 560

Score = 249 bits (635), Expect = 6e-65

Identities = 167/565 (29%), Positives = 282/565 (49%), Gaps = 58/565 (10%)

Query: 9 VIALLFVSFMIWQAWEQDKNPQPQAQQTQTTTTAAAGSAADQGV-----PASG----- 56
+IA + +S I W+ Q +Q Q T A + Q + PA+G

Sbjct: 8 LIAAIILSLSIIFGWQYFVVKPEQKKQQQQITVQKAENLKKQQLKALVEPATGIVVQAES 67

Query: 57 QGKLISVKTDVLDLTINTRGGDVEQALLPAYPKELNSTQPFQLL--ETSPQFIYQAQSGL 114
Q + I ++++ L +I+ +G + +L Y ++L+ P L + + Y A+ GL

Sbjct: 68 QVQRIKIESESLTGSISLKLGRFDDLILKKYKQDLSKNSPEVRLFSPANTENAYFAEVGL 127

Query: 115 TGRDGPDPNPANGPRPLYNVEKDAYVLAEGQNELQVPMYTDAGNTFTKTFLVLRGDYAV 174
N ++N D+ +L+ E V + + + G F T + +Y

Sbjct: 128 VSNLSSVKLPNNDT-IWN--SDSEILSP---EKPVHLFWVNEDGVKFLVTIAVDE-NYLF 180

Query: 175 NVNYNVQNAGEKPLEISSFGQLKQSITLPPHLDTGSSNFALHTFRGAAYSTPDEKEYEKYK 234
+ + N K L + S+G + + + A++ DE ++Y

Sbjct: 181 TIEQTIVNNSNKELPVQSYGLINRKYI-----AVEKAVNILHQGPICIDENLKEYS 232

Query: 235 FDTIADNENLNIS-SKGGWVAMLQQYFATAWIPH---NDGTNNFYTANLGNIAAIGYKS 290
+D I D ++ + SK W+ + +Y+ ++ IP N +N Y G + + S

Sbjct: 233 YDDIKDKKSEKFAASKVDWIGITDKYWLSSLIPDKSSNYSSNFNYALKQGTERYQVDFIS 292

Query: 291 QPVLVQPGQTGAMNSTLWVGPEIQDKMAAVAPHLDL-----TVDYGWLWFISQPLFKLLK 345
+++PG+ ++ S ++ G + D + D+ +D+GW + I++P+F +

Sbjct: 293 PVQIIKPGENFSIKSRIFAGAKKVDLLDKYEKQYDIKLFDRIDFGWFIITKPVFYAMN 352

Query: 346 WIHSFVGNWGFSSIIITFIVRGIMYPLTKAQYTSMAKMRMLQPKIQAMRERLGDDKQRIS 405
+ + +VGN+G SI+I+T I++ +M+ L Y SM KM+ LQP+I ++ DDK R++

Sbjct: 353 FFYGYVGNFGVSILIVTVIIKLLMFTLANKSYSRMKKMKNLQPEIDRIKNLYSDDKARLN 412

Query: 406 QEMMALYKAEKVNPLGGCFPLLIQMPIFLALYMLMGSVELRQAPFALWIHDLQAQDPYY 465
QE+MALYK EKVNP+ GC P+L+Q+P+F ++Y +L ++E+RQAPF WI DLSA DP

Sbjct: 413 QEIMALYKKEKVNVPVAGCLPILVQIPVFFSIYKVLYVTIEMRQAPFYGWIKDLSASDPTT 472

Query: 466 IL-----PILMGVTMFFIQKMSPTTVTDPMQQKIMTFMPVIFTVFF 506
I PILM +TMF QKMSP DPMQ ++M FMP+IF F

Sbjct: 473 IFNLFGLLPFSPPSFLMIGAWPILMAITMFLQQKMSPEP-ADPMQAQVMKFMPLIFLFMF 531

Query: 507 LWFPSGLVLYYIVSNLVTIIQQQLI 531
FP GL++Y+ +N+++IIQQ I

Sbjct: 532 SSFPVGLLIYWSWNNILSIIQQYYI 556

>ref|NP_220442.1| 60 KD INNER-MEMBRANE PROTEIN (yidC) [Rickettsia prowazekii str.
Madrid E]
Length = 560

Score = 248 bits (634), Expect = 7e-65

Identities = 168/566 (29%), Positives = 285/566 (50%), Gaps = 56/566 (9%)

Query: 6 NLLVIALLFVSFMI-WQAW----EQDKNPQPQAQQT-----QTTTTAAGSAADQGV PAS 55
 NL+ +L +S + WQ + EQ K Q A + Q A A+D V +
 Sbjct: 7 NLIAAVVLSLSIIFGWQYFFVKPEQKKQQQRIAMHKSENLNKQKLKALAEPASDIAVQEA 66

Query: 56 GQGKLISVKTDVLDLTINTRGGDVEQALLPAYPKELNSTQPFQLL--ETSPQFIYQAQSG 113
 Q + I +++++ L +I +G + +L Y ++L+ P L + + Y A+ G
 Sbjct: 67 SQVQRIKIESESLTGSIALKGLRFDDLILKKYKQDLSQNSPAVRLFSPANTENAYFAEIG 126

Query: 114 LTGRDGPDPNPANGPRPLYNVEKDAYVLAEGQNELQVPMYTDAGNTFTKTFVLKRGDYA 173
 L N P D+ VL+ E V + + + G F T + + +Y
 Sbjct: 127 LVSNL---NSVKLPNSNTVWNSDSEVLSP---EKPVNLFWINEDGIKFLVTITVDK-NYL 179

Query: 174 VNVNINYNQAGEKPLEISSFGQLKQSITLPPHLDTGSSNFALHTFRGAAYSTPDEKEYEKY 233
 + + N +K L + S+G + + S A++ DE ++Y
 Sbjct: 180 FTIEQTIINNSDKELPVQSYGLINRKYI-----SLEKAVNILHQGPICIDENLKEY 231

Query: 234 KFDTIADNENLNIS-SKGGWVAMLQQYFATAWIPHNDG--TNNF-YTANLGNIAAIGYK 289
 +D I D ++ + SK W+ + +Y+ ++ IP ++NF Y G + +
 Sbjct: 232 SYDDIKDKKSTKFALSKVDWIGITDKYWLSSLIPDKSSRYSSNFNYALKQGTERYQVDFI 291

Query: 290 SQPVLVQPGQTGAMNSTLWVGPEIQDKMAAVAPHLDL-----TVDYGWLWFISQPLFKLL 344
 S +++PG+ ++ S ++ G + D + D+ +D+GW + I++P+F +
 Sbjct: 292 SPVQVIKPGENLSIKSRIFAGAKKVDLLDEYEKSYDIKLFDRIDFGWFYIITKPVFYAM 351

Query: 345 KWIHSFVGNGWFSIIITFIVRGIMYPLTKAQYTSMAKMRMLQPKIQAMRERLGDDKQRI 404
 + + +VGN+G SI+I+T I++ +M+ L Y SM KM+ LQP+I ++ +DK R+
 Sbjct: 352 NFFYGYVGNFGISILIVTVIIKLLMFTLANKSYRSMKKMKNLQPEIDRIKNLYNNDKARL 411

Query: 405 SQEMMALYKAKEKNPLGGCFPLLIQMPIFLALYYMLMGSVELRQAPFALWIHDLQAQDPY 464
 +QE+MALYK EKNVP+ GC P+L+Q+P+F ++Y +L ++E+RQAPF WI DLS+ DP
 Sbjct: 412 NQEIMALYKKEKNPNVAGCLPILVQIPVFFSIYKVLYVTIEMRQAPFFGWIKDLSSPDPT 471

Query: 465 YIL-----PILMGVTMFFIQKMSPTTVTDPMQQKIMTFMPVIFTVF 505
 I PILM +TMF QKMSP + DP+Q ++M FMP+IF
 Sbjct: 472 TIFNLFGLLPFAPPSFLMIGAWPILMAITMFLHQKMSP-ELADPIQAQVMKFMPLIFLFM 530

Query: 506 FLWFPSGLVLYYIVSNLVTIIQQQLI 531
 F FP GL++Y+ +N+++IIQQ I
 Sbjct: 531 FSSFPVGLLIYWSWNNILSIIQQYYI 556

>ref|NP_359711.1| 60 kD inner-membrane protein [Rickettsia conorii str. Malish 7]
 Length = 560

Score = 248 bits (632), Expect = 1e-64

Identities = 166/565 (29%), Positives = 282/565 (49%), Gaps = 58/565 (10%)

Query: 9 VIALLFVSFMIWQAWQDKNPQPQAQQTQT-----PASG----- 56
 +IA + +S I W+ Q +Q Q A + Q + PA+G
 Sbjct: 8 LIAAIIISLSIIFGWQYFVVKPEQKKQQQIAVQKAENLKKQQLKALVEPATGIVVQEEES 67

Query: 57 QGKLISVKTDVLDLTINTRGGDVEQALLPAYPKELNSTQPFQLL--ETSPQFIYQAQSG 114
 Q + I +++++ L +I+ +G + +L Y ++L+ P L + + Y A+ GL
 Sbjct: 68 QVQRIKIESESLTGSISLKGLRFDDLILKKYKQDLSKNSPEVRLFSPANTENAYFAEVGL 127

Query: 115 TGRDGPDPNPANGPRPLYNVEKDAYVLAEGQNELQVPMYTDAGNTFTKTFLVLRGDIYAV 174
 N ++N D+ +L+ E V + + + G F T + +Y
 Sbjct: 128 VSNLSSVKLPNNDT-IWN--SDSEILSP---EKPVHLFWVNEDGVKFLVTITVDE-NYLF 180

Query: 175 NVNYNVQNAGEKPLEISSFGQLKQSITLPPHLDTGSSNFALHTFRGAAYSTPDEKEYEKYK 234
 + + N +K L + S+G + + + A++ DE ++Y
 Sbjct: 181 TIEQTIVNNSDKELPVQSYGLINRKYI-----AVEKAVNILHQGPICIDENLKEYS 232

Query: 235 FDTIADNENLNIS-SKGGWVAMLQYFATAWIPH---NDGTNNFYTANLGNIAAIGYKS 290
 +D I D ++ + SK W+ + +Y+ ++ IP N +N Y G + + S
 Sbjct: 233 YDDIKDKKSEKFAASKVDWIGITDKYWLSSLIPDKSSNYSSNFNYALKQGTERYQVDFIS 292

Query: 291 QPVLVQPGQTGAMNSTLWVGPEIQDKMAAVAPHLDL-----TVDYGWLWFISQPLFKLLK 345
 +++PG+ ++ S ++ G + D + D+ +D+GW + I++P+F +
 Sbjct: 293 PVQIIKPGENFSIKSRIFAGAKKVDLLDKYEKQYDIKLFDRIDFGWFYIITKPVFYAMN 352

Query: 346 WIHSFVGNWGFSSIIITFIVRGIMYPLTKAQYTSMAKMRMLQPKIQAMRERLGGDDKQRIS 405
 + + +VGN+G SI+I+T I++ +M+ L Y SM KM+ LQP+I ++ DDK R++
 Sbjct: 353 FFYGYVGNFGVSILIVTVIIKLLMFTLANKSYRSMKKMKNLQPEIDRIKNLYSDDKARLN 412

Query: 406 QEMMALYKAQKVNPLGGCFPLLIQMPIFLALYMLMGSVELRQAPFALWIHDLQAQDPYY 465
 QE+MALYK EKVNP+ GC P+L+Q+P+F ++Y +L ++E+RQAPF WI DLSA DP
 Sbjct: 413 QEIMALYKKEKVNPNVAGCLPILVQIPVFFSIYKVLYVTIEMRQAPFYGWIKDLSASDPTT 472

Query: 466 IL-----PILMGVTMFFIQKMSPTTVTDPMQKIMTFMPVIFTVFF 506
 I PILM +TMF QKMSP DPMQ ++M FMP+IF F
 Sbjct: 473 IFNLFGLLPFSPPSFLMIGAWPILMAITMFLQKMSPEP-ADPMQAQVMKFMPLIFLFMF 531

Query: 507 LWFPSGLVLYYIVSNLVTIIQQQLI 531
 FP GL++Y+ +N+++IIQQ I
 Sbjct: 532 SSFPVGLLIYWSWNNILSIIQQYYI 556

>ref|ZP_00192708.1| COG0706: Preprotein translocase subunit YidC [Mesorhizobium sp.
 BNC1]
 Length = 609

Score = 248 bits (632), Expect = 1e-64

Identities = 182/600 (30%), Positives = 287/600 (47%), Gaps = 82/600 (13%)

Query: 1 MDSQRNLLV-IALLFVSFMIWQAW-----EQDKNPQPQAQQTQTQTTTTAAGSAADQGV 52
 M++ RNLL+ IAL V +WQ + Q + Q +AQ+ +T AD
 Sbjct: 1 MENNRNLLITIALSVVILTLWQVFYVNPRVDAQREAAQIEAQAQETEEKLGTQGADIPA 60

Query: 53 PASGQGL-----ISVKTDVLDLTINTRGGDVEQALLPAYPK 89
 P + G +++ T L TIN G ++ LL Y
 Sbjct: 61 PGATPGSTAVPGSAIPRTQVTRQEALAGAERTVIDTIRLAGTINLAGARLDDLLLDYRV 120

Query: 90 ELNSTQP-FQLETS--PQFIYQAQSGLTGRDGPDPNPANGPRPLYNVEKDAYVLAEGQNE 146
 ++ P LL + P+ Y + G TG + GP ++ +++ + L+ G
 Sbjct: 121 TVDKDSPNIDLLGPAGLPEG-YFVEVGYTG-NASTGAVPGPDTVWQLQEGS-TLSPGS-- 175

Query: 147 LQVPMYTDAGNTFTKTFLVLRGDIYAVNVNYNVQNAGEKPLEISSFGQLKQSITLPPHL 206
 V +++T+ G TF +TF + +Y + ++NA +P+EI ++G+ T
 Sbjct: 176 -PVTLSFTNDRGLTFLRTFAVDE-NYLFITITDIRNAAGEPVEIRNYGR-----TTRFGQ 228

Query: 207 DTGSSNFALHTFRGAAYSTPDEKEYEKYKFDTIA-DNENLNISKGGWVAMLQYFATAWI 265
 + + LH G +E + + T D + L S GW+ + +Y+A +
 Sbjct: 229 PKTAGIYILH--EGFIGVLGEEGLREVDYSTAQEDGQVLPKGSADGWLGITDKYWAVTMV 286

Query: 266 PH--NDGTNNFYTANLGNIAAIGYKSPVLVQPGQTGAMNSTLWVGP-EIQDKMAAVAP 322
P D F + G Y + PV V PG + + ++ G E+ A
Sbjct: 287 PRAQKDFEPFAYFSDGRERYQADYLTDPVTVAPGGEAKIETLVFAGAKEVHVVDAYETQ 346

Query: 323 H----LDLTVDYGWLWFISQPLFKLLKWIHSFVGNWGFSSIIITFIVRGIMYPLTKAQYT 378
H +L +D+GW +FI++P+F L+ W+ +GN+G +I+ T V+ + +PL Y
Sbjct: 347 HNIRQFELLIDWGWFYFITKPMFYLLIDWLFRLGNFGVAILATTVFVKLVFFPLANKSYK 406

Query: 379 SMAKMRMLQPKIQAMRERLGDDKQRISEMMALYKAQKVNPLGGCFPLLIQMPIFLALYY 438
SMA M+ +QP + +RE+ DDK + Q MM LYK EK+NPL GC+P+LIQ+P+F ALY
Sbjct: 407 SMANMKKVQPALLEIREKYADDKMKQQQAMMELYKKEKINPLAGCWPILIQIPVFFALYK 466

Query: 439 MLMGSVELRQAPFALWIHDLSAQDPYYIL-----PILMGV 473
+L ++E+R APF WI DLSA DP I PI+MG+
Sbjct: 467 VLYVTIEMRHAPFFGWIQDLSAPDPTTIFNLFGLLPDPSQVPVFGPFLMLGVWPIIMGI 526

Query: 474 TMFFIQKMSPTTIVTDPMQQKIMTFMPVIFTVFFLWFPSGLVLYYIVSNLVTIIQQQLIYR 533
TMF +M+PT DP Q I +MPVIFT FP+GLV+Y+ +NL++IIQQ +I +
Sbjct: 527 TMFLQMRMNPTP-PDPTQAMIFNWMPVIFTFMLATFPAGLVIYWAWNNLLSIIQQGVIMK 585

>ref|YP_064591.1| conserved hypothetical membrane protein [Desulfotalea psychrophila
LSv54]
Length = 553

Score = 246 bits (627), Expect = 5e-64

Identities = 187/571 (32%), Positives = 285/571 (49%), Gaps = 55/571 (9%)

Query: 1 MDSQRNLLVIALLFVSMIWAWEQDKNPQQAQQTQTOTTTTAAGSAADQG----- 51
M+++R LL I + F +Q + + QP Q T++T TT G++A Q
Sbjct: 1 METKRALLAIVISFAILFGYQYFFPGLD-QP-VQTTSETQTTVNGTSAKQAGAIQEITAP 58

Query: 52 -VPASGQGL-----ISVKTDVLDLTINTRGGDVEQALLPAYPKELNSTQP--FOLLET 102
+P K I V TD+ TI+ GG ++ +L KE N+ QL+
Sbjct: 59 VIPVVASAKYDRVPRDIVVDTDLTYATISEAGALKSFVLKEQ-KETNAEDSPGMQLVNN 117

Query: 103 SPQFIYQAQSGLTGRDGPDPNPANGPRPLYNVEKDAYVLAEGQNELQVPMTYTDAAGNTFT 162
S Y LT G P+N L +D+ V + ++ MT + G
Sbjct: 118 SKTDGYP----LTFWGGGAAPSN----LLYTSQDSEVRFGSNGKARLIMTAKSSTGLVIE 169

Query: 163 KTFVLKRGDYAVNVNYNVQNAGEKPLEISSFGQLKQSITLPPHLDTGSSNFALHTFRGAA 222
+ + + Y +++ V N + L+ S+ QL Q P+ T + A F G
Sbjct: 170 RYVTFDKKTYLFDLDVRVNVNSGQALQGS--QLHQVSV--PYESTEDNPAARFLFMGPV 225

Query: 223 YSTPDEKEYEKYKFDTIADNENLNISCKGGWVAMLQQYFATAWIPHNNGTNNFYT--ANL 279
E E D ++ + W+ +YF + +P+ F T A+L
Sbjct: 226 VYADGELTEIDPKDL--EDGPQSFMGDIQWLGYESRYFMSMIVPYGLDQTFTTSGGADL 283

Query: 280 GNGIAAIGYKSPVLVQPGQTGAMNSTLWVGPEIQDKMAAVAPHLDLTVDYGWLWFISQP 339
A G + + G + GP+ + + + LD V++GW I++P
Sbjct: 284 TKSFIAGGLDT----LAAGAEKEYKYHVLYGPKKVEMLKSAGYDLKAVNFGWFDIIAKP 339

Query: 340 LFKLLKWIHSFVGNWGFSSIIITFIVRGIMYPLTKAQYTSMAKMRMLQPKIQAMRERLGD 399
LL + HSF N+G +II++T + +GI +P+T+ SM M+ LQPK+ A++E+ D
Sbjct: 340 TLWLLNFFHSFTHNYGIAIILVTIMFKGIFWPITQKGMKSMKNMQKLQPKMAALKEKHKD 399

Query: 400 DKQRISEMMALYKAQKVNPLGGCFPLLIQMPIFLALYYMLMGSELVRQAPFALWIHDLS 459
D R+++E+M+LYKA KVNPLGGC P+++Q+P+F ALY +L+ S+ELR APF WI DLS

Sbjct: 400 DPTRMNKEVMSLYKAYKVNPLGGCLPMVLQIPVFFALYKVLLLSIELRHAPFMFWITDLS 459

Query: 460 AQD-----PYY----ILPILMGVTMFFIQKMSPTTVTDPMQQKIMTFMPVIFTVFFL 507
A D PY +L +LMG +MF QK SPTT DP Q KIM F+PV+FT FL

Sbjct: 460 APDRLWIGFNLPLYLGGLPVLTLLMGASMFLQQKFSPTT-ADPTQAKIMMFLPVVFTFMFL 518

Query: 508 WFPSGLVLYYIVSNLVTIIQQQLIYRGLEKR 538
F SGLVLY+ V+NL++I+QQ LI R ++ +

Sbjct: 519 NFASGLVLYWVFNLLSILQQVLINRDVKHK 549

>ref|NP_774738.1| blr8098 [Bradyrhizobium japonicum USDA 110]
Length = 616

Score = 246 bits (627), Expect = 5e-64
Identities = 171/572 (29%), Positives = 275/572 (48%), Gaps = 76/572 (13%)

Query: 21 QAWEQDKNPQQAQQTQTOTTTTAAGSAADQGV PASGQ-----GKLISVKTD 66
QA Q PQP A T T +G AA PA+GQ + + T

Sbjct: 41 QAELQKTTPTAS-ATPGATPQSGGAAQPSTPAAGQQAQPVVARDAAIAASPRVKIDTP 99

Query: 67 VLDLTINTRGGDVEQALLPAYPKELNSTQPFOLLETSPQFI---YQAQSGLTGRDGPDPNP 123
+ +I+ +GG ++ L Y + ++ P ++ SP Y A+ G G

Sbjct: 100 RIAGSISLKGGRIDVALVQYRETVPKSP-PIVLYSPSGTAEPYAEEFGWVPATGV TAK 158

Query: 124 ANGPRPLYNVEKDAYVLAEGQNELQVPMTYTDAAGNTFTKTFVLKRGDYAVNVNYNVQNA 183
+ L+ + + L+ + + G TF +T + Y + V N

Sbjct: 159 LPDAQTLWQQDGSGSLTPTTPAVLK---WDNGEGLTFRRTISVD-DHYLFTIKDEVS NV 213

Query: 184 GEKPLEISSFGQLKQSITLPPHLDTGSSNFALHTFRGAAYSTPDEKYEKYKFDTIADNEN 243
G P+ + F + + T P + S + LH + ++Y + I + ++

Sbjct: 214 GNAPVTLYPFALISRHGT--PQV---SGYYILHEGLIGYL----DGLQEYAYKKIDEAKS 264

Query: 244 LNISSKGGWVAMLQQYFATAWIPHNDGT--NNFYTANLGN-GIAAIGYKSQPVLVQPGQT 300
+N + GW+ M +Y+A+A +P F + +GN Y PV V G +

Sbjct: 265 VNFKATNGWLGMTDKY WASALLPDTSAQLQARFSSNPVGNVHTYQTDYLLDPVTVAIGGS 324

Query: 301 GAMNSTLWVGPEIQDKMAAVAP-----HLDLTVDYGWLWFISQPLFKLLKW 346
N+ L+ G + + P H DL +D+GW +FI++P+F L +

Sbjct: 325 ATANARLFAGAKEAGVVGINFPLAGHGGYNKELNLNHFLLIDWGWFYFITKPMFLGLDF 384

Query: 347 IHSFVGNWGFSSIIITFIVRGIMYPLTKAQYTSMAKMRMLQPKIQAMRERLGDDKQRISQ 406
+ F GN+G SI+++T IV+ + +PL Y SMAKM+ +QP++QA++ER DDK + Q

Sbjct: 385 FYRFFGNFGISILLVTIVIKLLFFPLANKSYASMAKMKSIPQLQALKERYPDDKVKQQQ 444

Query: 407 EMMALYKAEKVNPLGGCFPLLIQMPIFLALYYMLMGSVELRQAPFALWIHDL SAQDP--- 463
EMM +Y+ EK+NP+ GC P++IQ+P+F +LY +L ++E+RQAPF WI DLSA DP

Sbjct: 445 EMMEIYRKEKINPVAGCLPVVIQIPVFFSLYKVLVFTIEMRQAPFYGWIKDLSAPDPTNL 504

Query: 464 -----YY----ILPILMGVTMFFIQKMSPTTVTDPMQQKIMTFMPVI 501
+Y I PI+MG+TM+F K++PT DP QQ I +MP+I

Sbjct: 505 FNLFGLIPLDPTTIPVFGHYLALGIWPIIMGITMWFQMKLNPTP-PDPTQQMIFNWMPLI 563

Query: 502 FTVFFLWFPSGLVLYYIVSNLVTIIQQQLIYR 533
FT FP+GLV+Y+ +N ++++QQ I R

Sbjct: 564 FTFMLAGFPAGLVIIYAWNNNTLSVLQQSFIMR 595

>ref|ZP_00153141.1| COG0706: Preprotein translocase subunit YidC [Rickettsia rickettsii]
Length = 560

Score = 246 bits (627), Expect = 5e-64
Identities = 166/565 (29%), Positives = 282/565 (49%), Gaps = 58/565 (10%)

Query: 9 VIALLFVSFMIWQAWQDKNPQQAQQTQTTTTAAGSAADQGV-----PASG----- 56
+IA + +S I W+ Q +Q Q A + Q + PA+G
Sbjct: 8 LIAAIILSLSIIFGWQYFVVKPEQKKQQQIAVQKAENLKKQQLKALVEPATGIVVQEEES 67

Query: 57 QGKLISVKTDVLDLTINTRGGDVEQALLPAYPKELNSTQPFQLL--ETSPQFIYQAQSG 114
Q + I +++ L +I+ +G + +L Y ++L+ P L + + Y A+ GL
Sbjct: 68 QVQRIKIESESLTGSISLKLRFDDLILKKYKQDLSKNSPEVRLFSPANTENAYFAEVGL 127

Query: 115 TGRDGPDPNPANGPRPLYNVEKDAYVLAEGQNELQVPMTYTDAAGNTFTKTFVLKRGDYAV 174
N ++N D+ +L+ E V + + + G F T + +Y
Sbjct: 128 VSNLSSVKLPNNDT-IWN--SDSEILSP---EKPVHLFWVNEDGVKFLVTITVDE-NYLF 180

Query: 175 NVNYNVQNAGEKPLEISSFGQLKQSITLPPHLDTGSSNFALHTFRGAAYSTPDEKEYEKYK 234
+ + N +K L + S+G + + + A++ DE ++Y
Sbjct: 181 TIEQTIVNNSDKELPVQSYGLINRKYI-----AVEKAVNILHQGPICIDENLKEYS 232

Query: 235 FDTIADNENLNIS-SKGGWVAMLQYFATAWIPH---NDGTNNFYTANLGNIAAIGYKS 290
+D I D ++ + SK W+ + +Y+ ++ IP N +N Y G + + S
Sbjct: 233 YDDIKDKKSEKFAASKVDWIGITDKYWLSSLIPDKSSNYSSNFYALKQGIERYQVDFIS 292

Query: 291 QPVLVQPGQTGAMNSTLWVGPEIQDKMAAVAPHLDL-----TVDYGWLWFISQPLFKLLK 345
+++PG+ ++ S ++ G + D + D+ +D+GW + I++P+F +
Sbjct: 293 PVQIIKPGKNFSIKSRIFAGAKKVDLLDKYEKQYDIKLFDRIDFGWFYIITKPVFYAMN 352

Query: 346 WIHSFVGNWGFSSIIITFIVRGIMYPLTKAQYTSMAKMRMLQPKIQAMRERLGDDKQRIS 405
+ + +VGN+G SI+I+T I++ +M+ L Y SM KM+ LQP+I ++ DDK R++
Sbjct: 353 FFYGYVGNFVGSILIVTVIIKLLMFTLANKSYRSMKKMKNLQPEIDRIKNLYSDDKARLN 412

Query: 406 QEMMALYKAQKVNPLGGCFPLLIQMPIFLALYYMLMGVELRQAPFALWIHDLAQPDPY 465
QE+MALYK EKVNP+ GC P+L+Q+P+F ++Y +L ++E+RQAPF WI DLSA DP
Sbjct: 413 QEIMALYKKEKVNVPVAGCLPILVQIPVFFSIYKVLYVTIEMRQAPFYGWIKDLSAPDPTT 472

Query: 466 IL-----PILMGVTMFFIQKMSPTTVTDPMQKIMTFMPVIFTVFF 506
I PILM +TMF QKMSP DPMQ ++M FMP+IF F
Sbjct: 473 IFNLFGLLPFAPPSFLMIGAWPILMAITMFLQKMSPEP-ADPMQAQVMKFMPLIFLFMF 531

Query: 507 LWFPGLVLYYIVSNLVTIIQQQLI 531
FP GL++Y+ +N+++IIQQ I
Sbjct: 532 SSFPVGLLIYWSWNNILSIIQQYYI 556

>ref|ZP_00346395.1| COG0706: Preprotein translocase subunit YidC [Desulfovibrio desulfuricans G20]
Length = 413

Score = 244 bits (622), Expect = 2e-63
Identities = 118/290 (40%), Positives = 186/290 (64%), Gaps = 11/290 (3%)

Query: 252 WVAMLQYFATAWIPHNDGTNNFYTANLGNIAAIGYKSQPVLVQPGQTGAMNSTLWVGP 311
W ++ YF P + L G+ ++ + + G + ++GP
Sbjct: 125 WGGVMCNYFMAVMAPEGALP--FKGVLEGGVYRSVVENSLSIASGSSAEFGIGYYIGP 182

Query: 312 EIQDKMAAVAPHLDLTVDYGWLWFISQPLFKLLKWIHSFVGNWGFSSIIITFIVRGIMYP 371
+ D++AA+ HLD ++YGW F+++PL LK+ +S+ GN+G +III+T +V+ + +P
Sbjct: 183 KESDRLAAMPYHLDEALNYGWFTFLAKPLVSGLKFFYSYAGNYGVAIILITLVKLLFWP 242

Query: 372 LTKAQYTSMAKMRMLQPKIQAMRERLGDDKQRISQEMMALYKA EKVNPLGGCFPLLIQMP 431
L++ Y SM +M+ LQP +Q ++E+ GDD+QR++QE+M LYK KVNPGGC P+L+Q+P
Sbjct: 243 LSQKSYKSMEQMKKLQPMVQKIKEYGDDRQRMNQEVMELYKTYKVNPAAGCLPMLLQIP 302

Query: 432 IFLALYYMLMGSVELRQAPF-----ALWIHDLAQDPYYILPILMGVTMFFIQKMSP 483
+FL LY L+ ++ELR APF +W+ DLSA+DP+YI P++MG TM Q+++P
Sbjct: 303 VFLGLYQGLLNAIELRHAPFIAHLPTDIVWLADLSAKDPFYITPVVMGATMLLQQLTP 362

Query: 484 TTVTDPMQQKIMTFMPVIFTVFLLWFPSGLVLYYIVSNLVTIIQQQLIYR 533
DP Q KIM FMPV+FT FL FP+GLV+Y++V+N+++I QQ + R
Sbjct: 363 AP-ADPTQAKIMMFMPVVFTFMFLNFPAGLVVYWLNNVLSIGQQWWMLR 411

>ref|ZP_00304958.1| COG0706: Preprotein translocase subunit YidC [Novosphingobium
aromaticivorans DSM 12444]
Length = 600

Score = 243 bits (620), Expect = 3e-63

Identities = 171/581 (29%), Positives = 285/581 (49%), Gaps = 66/581 (11%)

Query: 1 MDSQRNLLV-IALLFVSFMIWQAWEQDKNPQPAQQTQTQTTTAAGSAADQ-----GV 52
M +QRNL++ + L + + W + PQP + + +A + ++ G+
Sbjct: 1 MQNQRLIMAVVLTGILLGLGWDVAMRWFYPQPAQPKVEAAASAEPANGEKPKRTREGGL 60

Query: 53 PASGQ-----GKLISVKTDVLDLTINTRGGDVEQALLPAYPKELN-STQPF 97
+G G I++ L +IN +G V+ L + + ++ ++ P
Sbjct: 61 QNAGDIALEKKDLAQELAAGHRIAIDAPGLKGSINLKGALVDDVTLARHREGVDRNSAPV 120

Query: 98 QLLETS-PQFIYQAQSGLTGRDGPDPNPANGPRPLYNVEKDAYVLAEGQNELQVPMTYTDA 156
+L + + AQ G G AN ++ + A+ + V + +T+A
Sbjct: 121 RLFSPAGTPAQHFAQIGWVGEGVAAPDAN---TMWQADG-----AKLTPQTPVTLRWTNA 172

Query: 157 AGNTFTKTFVLKRGDYAVNVNYNVQNAGEKPLEISSFGQLKQSITLPPHLDTGSSNFALH 216
+G T++ + + GDY + V N G P+ + F + ++ D +S +
Sbjct: 173 SGQTYISIRYAIID-GDYMITATQGVANTGPAPVVVRPFALVNRT-----DKTASLDTWN 224

Query: 217 TFRGAAYSTPDEKEYEKYKFDTIADNENLNISSKG--GWVAMLQQYFATAWIPHNDGTNNF 274
G + + T+A+ E I KG W+ Y+ +A IP +
Sbjct: 225 VHSGPIGAFDGSVNFNNDNYSTVAEAEAGGAIPFKGTANWIGFTDIYWLSALIPDANAKAEA 284

Query: 275 YTANLNGIAAIGYKSQPVLVQPGQTGAMNSTLWVGPE----IQDKMAAVAPHLDLTVDY 330
+LG G+ V + PG+ + L+ G + ++ AA + L++D+
Sbjct: 285 AFRSLGQGVYRADLIYPSVSIAPGKALSQTVRLFAGGKENAVLEKYEAGVTNFSLSIDW 344

Query: 331 GWLWFISQPLFKLLKWIHSFVGNWGFSSIIITFIVRGIMYPLTKAQYTSMAKMRMLQPKI 390
GW + +P+F LL I VGN+G +II+T IVRG+M+P+ + Q+ SMA MR LQPK+
Sbjct: 345 GWFRWFEKPIFWLLDSIFKKVGNGFVAILLLTLIVRGVMFPIAQRQFASMAAMRALQPKM 404

Query: 391 QAMRERLGDDKQRISQEMMALYKA EKVNPLGGCFPLLIQMPIFLALYYMLMGSVELRQAP 450
+A++ER DDKQ+ QE+M LYK EKVNPL GC P+ +Q+P+F ALY +L+ ++E+R P
Sbjct: 405 KAIQERYKDDKQKQKQQEIMELYKREKVNPLAGCLPIFLQIPVFFALYKVLVLTIEMRHQP 464

Query: 451 FALWIHDLAQDPYY-----ILPILMGVTMFFIQKMSPTTVTDPMQ 491
FALWI DLSA DP + +L IL+G+TM+ K+ P + DP Q
Sbjct: 465 FALWIKDLSAPDPLHVLNLFGLLPDPSPFLGIGVLAILLGITMWLQFKLQPAAM-DPAQ 523

Query: 492 QKIMTFMPVIFTVFFLWFPSGLVLVYIVSNLVTIIQQQLIY 532
 Q++ FMP I F +GL++Y+I SNL+TI QQ+ +Y
 Sbjct: 524 QQVFAFMPWIMMFVMAPFAAGLLIYWITSNLLTIAQQKYLY 564

>ref|NP_208241.1| 60 kDa inner-membrane protein [Helicobacter pylori 26695]
 Length = 547

Score = 242 bits (617), Expect = 7e-63
 Identities = 123/336 (36%), Positives = 208/336 (61%), Gaps = 18/336 (5%)

Query: 216 HTFRGAAYSTPDEKYEKFKDFTIADNENLNISSEKGGWVAMLQQYFATAWIPHN-DGTNNF 274
 +TF G D+K EK + D + + S +++ + +YF T + G
 Sbjct: 225 YTFSGVLLNSDKKIEKIEDK---DAKEIKRFSNTLFLSSVDRYFTTLLFTKDPQGFEAL 281

Query: 275 YTANLG--NGIAAIGYKSQPVLVQPGQTGAMNSTLWVGPEIQDKMAAVAPHLDLTVDYGW 332
 + +G N + I K++ N ++GP+ + A++P L ++YG
 Sbjct: 282 IDSEIGTKNPLGFISLKNEA-----NLHGYIGPKDYRSLKAISPMLTDVIEYGL 330

Query: 333 LWFISQPLFKLLKWIHSFVGNWGFSSIIITFIVRGIMYPLTKAQYTSMAKMRMLQPKIQA 392
 + F ++ +F LL +++ FVGNWG++II++T IVR I+YPL+ SM K++ L PK++
 Sbjct: 331 ITFFAKGVFVLLDYLYQFVGNWGWAILLLTIIVRIILYPLSYKGMVSMQKLKELAPKMKE 390

Query: 393 MRERLGDDKQRISEMMALYKAEKVNPLGGCFPLLIQMPIFLALYYMLMGSVELRQAPFA 452
 ++E+ + Q++ MM LYK NPLGGC PL++Q+P+F A+Y +L +VEL+ + +
 Sbjct: 391 LQEKYKGEPQKLQAHMMQLYKKHGANPLGGCLPLILQIPVFFAIYRVLYNAVELKSSEWI 450

Query: 453 LWIHDLSAQDPYYILPILMGVTMFFIQKMSPTTVTDPMQQKIMTFMPVIFTVFFLWFPSG 512
 LWIHDLS DPY+ILP+LMG +M++ Q ++P T+TDPMQ KI +P++FT+F + FP+G
 Sbjct: 451 LWIHDLSIMDPYFILPLLGMASMYWHQSVTPNTMTDPMQAKIFKLLPLLFTIFLITFPAG 510

Query: 513 LVLVYIVSNLVTIIQQQLIYRGLE-KRGLHSREKKK 547
 LVLY+ +N+++++QQ +I + LE K+ +H++ KK+
 Sbjct: 511 LVLYWTTNNILSVLQQLIINKVLENKKRMHAQNKKE 546

>ref|NP_907465.1| 60 KDA INNER-MEMBRANE PROTEIN [Wolinella succinogenes DSM 1740]
 Length = 536

Score = 241 bits (614), Expect = 2e-62
 Identities = 110/231 (47%), Positives = 164/231 (70%)

Query: 308 WVGPEIQDKMAAVAPHLDLTVDYGWLWLFISQPLFKLLKWIHSFVGNWGFSSIIITFIVRG 367
 ++G + + ++ P L V+YG++ F ++PLF LL W++ F GNWG++I+++T +VR
 Sbjct: 293 YIGAKDFRLLESIYPSLTDVVEYGFITFFAKPLFLLLDWLYKFCGNWGWAIVLLTLVVRI 352

Query: 368 IMYPLTKAQYTSMAKMRMLQPKIQAMRERLGDDKQRISEMMALYKAEKVNPLGGCFPLL 427
 I++PLT SM K++ + PK++ ++E+ D Q++ MM LYK NP+GGC PLL
 Sbjct: 353 ILFPLTYKGMVSMQKLKDIAPKMKEIQEKYKGDQPQLQVHMMELYKKHGANPMGGCLPLL 412

Query: 428 IQMPIFLALYYMLMGSVELRQAPFALWHDLSAQDPYYILPILMGVTMFFIQKMSPTTVT 487
 +QMPIF A+Y +L ++EL+ A + LWI+DLS DPY+ILPILMG +MF Q ++PTT T
 Sbjct: 413 LQMPIFFAIYRVLYNAIELKGADWILWINDLSVMDPYFILPILMGASMFLQQLHTPTTFT 472

Query: 488 DPMQQKIMTFMPVIFTVFFLWFPSGLVLVYIVSNLVTIIQQQLIYRGLEKR 538
 DPMQ+K+ F+P+IFT FF+ FPSGLVLY+ VSN+ +I QQ I + LE +
 Sbjct: 473 DPMQEKVFKFLPLIFTFFFVTFPSGLVLYWFVSNVFSIAQQLFINKTLEAK 523

>ref|NP_224061.1| putative Inner membrane protein [Helicobacter pylori J99]
Length = 549

Score = 237 bits (605), Expect = 2e-61

Identities = 122/336 (36%), Positives = 205/336 (61%), Gaps = 18/336 (5%)

Query: 216 HTFRGAAYSTPDEKYEKYKFDTIADNENLNISSEKGGWVAMLQQYFATAWIPHN-DGTNNF 274
+TF G D+K EK + D + + S +++ + +YF T + G
Sbjct: 228 YTFSGVLENTDKKIEKIEDK---DAKEIKRFSNTLFLSSVDRYFTTLLFTKDPQGFEAL 284

Query: 275 YTANLG--NGIAAIGYKSQPVLVQPGQTGAMNSTLWVGPEIQDKMAAVAPHLDLTVDYGW 332
+ +G N + I K++ N ++GP+ + A++P L ++YG
Sbjct: 285 IDSEIGTKNPLGFISLKNEA-----NLHGYIGPKDYRSLKAISPMLTDVIEYGL 333

Query: 333 LWFISQPLFKLLKWIHSFVGNWGFSSIIITFIVRGIMYPLTKAQYTSMAKMRMLQPKIQA 392
+ F ++ +F LL +++ FVGNWG++II++T IVR I+YPL+ SM K++ L PK++
Sbjct: 334 ITFFAKGVFVLLDYLYQFVGNWGWAIILLTIIIRIILYPLSYKGMVSMQKLKELAPKMKE 393

Query: 393 MRERLGDDKQRISQEMMALYKAQKVNPLGGCFPLLIQMPIFLALYYMLMGSVELRQAPFA 452
++E+ + Q++ MM LYK NPLGGC PL++Q+P+F A+Y +L +VEL+ + +
Sbjct: 394 LQEKYKGEPQKLQAHMMQLYKKHGANPLGGCLPLILQIPVFFAIYRVLYNAVELKSSEW 453

Query: 453 LWIHDLSAQDPYYILPILMGVTMFFIQKMSPTTVDPMQQKIMTFMPVIFTVFFLWFPSG 512
LWIHDLS DPY+ILP+LMG +M++ Q ++P T+TDPMQ KI +P++FT+F + FP+G
Sbjct: 454 LWIHDLSIMDPYFILPLLMGASMYWHQSVTPNTMTDPMQAKIFKLLPLLFTIFLITFPAG 513

Query: 513 LVLYYIVSNLVTIIQQQLIYRGLE-KRGLHSREKKK 547
LVLY+ N+++++QQ +I + LE K+ H++ K+
Sbjct: 514 LVLYWTTNLSVLQQLIINKVLENKKRAHAQNIKE 549

>ref|NP_970612.1| 60 KD inner-membrane protein [Bdellovibrio bacteriovorus HD100]
Length = 539

Score = 232 bits (592), Expect = 5e-60

Identities = 129/334 (38%), Positives = 196/334 (58%), Gaps = 19/334 (5%)

Query: 214 ALHTFRGAAYSTPDEKYEKY-----KFDTI----ADNENLNISSEKGGWVAMLQQYFAT 262
++HT ++ P +++ + K DT+ A + + V++ QYFA
Sbjct: 202 SIHTHASTSFLFPSYEQDFVTHNGGKHDTVNFSGATEDVVKDFPATSLVSVSSQYFAA 261

Query: 263 AWIPHN DGTNNFYT---ANLGNIAAIGYKSQPVLVQPGQTGAMNSTLWVGPEIQDKMAA 319
A + ++ N +A + YK P V+P T + + GP+ D + A
Sbjct: 262 AILDKSEIMPEVKLNAQINAKTAMAEVYK--PASVKPEMT--FSEVYFAGPKSIDALKA 317

Query: 320 VAPHLDLTVDYGWLWLFISQPLFKLLKWIHSFVGNWGFSSIIITFIVRGIMYPLTKAQYTS 379
V P + +D+G+ FI++PL ++K HS VGNWGF+III+T +VR + P + S
Sbjct: 318 VDPEMASLIDFGFFGFIARPLLYVMKAAHSVGNWGFATIIITLLVRLCVLPFNIMSFKS 377

Query: 380 MAKMRMLQPKIQAMRERLGDDKQRISQEMMALYKAQKVNPLGGCFPLLIQMPIFLALYYM 439
M M+ +QP IQ +RE+ +D R++QEMMA+ K NPLGGC P+L+Q+P+F ALY +
Sbjct: 378 MKAMQKVQPIIQGLREKYKEDPMRLNQEMMAVMKQNGANPLGGCLPMLLQIPVFFALYRV 437

Query: 440 LMGSVELRQAPFALWHDLSAQDPYYILPILMGVTMFFIQKMSPTTVDPMQQKIMTFMP 499
+ S+EL +PF LWI DLS+ D +Y+LP+ M V M+ QK++P+T+ DP Q KIM F+P
Sbjct: 438 IGSSIELYNSPFILWITDLSHDKFYVLPVSMVFMVYIQQKITPSTM-DPTQAKIMAFPL 496

Query: 500 VIFTVFFLWFPSGLVLYIIVSNLVTIIQQQLIYR 533
 V+F++F L P+GL LY +VS L IIQQ LI R
 Sbjct: 497 VVFSLFMLQLPAGLTLYMVVSTLFGIIQQWLIMR 530

>ref|NP_945985.1| 60 kDa inner membrane protein [Rhodopseudomonas palustris CGA009]
 Length = 622

Score = 232 bits (591), Expect = 7e-60

Identities = 172/608 (28%), Positives = 278/608 (45%), Gaps = 91/608 (14%)

Query: 2 DSQRNLLVIALLFVSFMIWQ-----AWEQDKNPQPQAQQTQTQTTTTAAGSAAD 49
 D++ +L + L + + WQ A +Q + + Q TQT A+ +AA
 Sbjct: 3 DNRNTILAVVLSGLVLLGWQYFFNIPQMEKQRAAQQAAQQAAKQQAETQTTPGAASPAAP 62

Query: 50 QG-----VPASGQ-----GKLISVKTDVLDLTINTRGGDVEQALLPAY 87
 PAS Q G I V+T L +I +G ++ L Y
 Sbjct: 63 AAPGAPGSAPASPPQAPAAAPTVSREAALAAGPRIKVETPRLSGSIALKGARIDDLALMQY 122

Query: 88 PKELN-STQPFQLETSPOFI-YQAQSGLTGRDGPDPNPANGPRPLYNVEKDAYVLAEGQN 145
 + ++ + P +L S Y A+ G G G L+ E +
 Sbjct: 123 RETVDPKSPPIELFSPSGSARPYAEFGWGAAGASVKLPDHNTLWEQEGTGALTPANP- 181

Query: 146 ELQVPMTYTDAGNTFTKTFVLKRGDYAVNVNYNVQNAGEKPLEISSFGQLKQSITLPPH 205
 V + + + G TF + + Y V +V N G P+ + F + + T PH
 Sbjct: 182 ---VTLKWDNGEGLTFRRQITVD-DRYLFTVKDDVTNTGGAPVTLYPFALISRHGT--PH 235

Query: 206 LDTGSSNFALHTFRGAAYSTPDEKYEKYKFDTIADNENLNISSKGGWVAMLQQYFATAWI 265
 ++ + LH G D+ ++Y + I + +++ + GW+ + +Y+A+A +
 Sbjct: 236 VE---GYIILH--EGLIGYLGDLQGLQEYSYSKIDEAKSVGFKATNGWLGITDKYWASALL 290

Query: 266 PHNDGT--NNFYTANLGNIA-AIGYKSPVLVQPGQTGAMNSTLWVGPEIQDKMAAVAP 322
 P F +GN Y V G T N+ L+ G + + P
 Sbjct: 291 PDTSAQLQARFSANKVGNVTYQTDYLEDARTVPIGGTVTANARLFAGAKEARVVGINFP 350

Query: 323 -----HLDLTVDYGWLWFISQPLFKLLKWIHSFVGNWGFSSIIITFIVRGI 368
 H DL +D+GW +FI++P+F L + VGN+G +I+++T +V+ +
 Sbjct: 351 FAGLGGYDRQLGLNHFDLLIDWGWFFYFITKPMFLALDFFFHLVGNFGVAILLVTVLVKLL 410

Query: 369 MYPLTKAQYTSMAKMRMLQPKIQAMRERLGDDKQRISQEMMALYKAQKVNPLGGCFPLLI 428
 PL Y SMAKM+ +QP++ A++ER DDK + QEMM +Y+ EK+NP+ GC P+L+
 Sbjct: 411 FLPLANKSYASMAKMKAIQPQLAALKERHPDDKVQKQEMMEIYRKEKINPVAGCLPILL 470

Query: 429 QMPIFLALYYMLMGSVELRQAPFALWIHDLQAQDP-----YYI 466
 Q+P+F +LY +L ++E+R APF WIHDLA DP Y +
 Sbjct: 471 QIPVFFSLYKVLVFTIEMRHAPFFGWIHDLAPDPTNIFNLFGLIPYDPTAIPVLGHYLV 530

Query: 467 L---PILMGVTMFFIQKMSPTTVDPMQQKIMTFMPVIFTVFFLWFPSGLVLYIIVSNLV 523
 L P++MG TM+F K++P DP QQ I +MPVIFT FP+GLV+Y+ +N +
 Sbjct: 531 LGAWPLVMGFTMWFQMKLNPPQ-PDPTQQMIFAWMPVIFTFMLAHFPAGLVIYWAWNNTL 589

Query: 524 TIIQQQLI 531
 ++ QQ I
 Sbjct: 590 SVAQQAQFI 597

>ref|ZP_00207261.1| COG0706: Preprotein translocase subunit YidC [Rhodobacter

sphaeroides 2.4.1]
Length = 623

Score = 229 bits (584), Expect = 5e-59

Identities = 174/596 (29%), Positives = 281/596 (47%), Gaps = 77/596 (12%)

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Query: 1  MDSQRNLLVIA--LLFVSFMIWQAWQDKNPQQAQQTQTQTTTTAAGSAADQGVPSAG-- 56
          MD Q  L++A  L F+  M+W          + + T  T  TA  +A  P  +
Sbjct: 1  MDDQNKNLILATGLSFLVIMVWFFLFPPPEAVTEGEPTVATQQTAVAPSATPDAPTTAVP 60

Query: 57  -----QGKLISVKTDVLDLTINTRGGDVEQALLPAYPKELN-STQPFQLLETSPQ-FIY 108
          + + + + T  L  +I+  GG ++  L +Y + L+  +Q  +LL  Q  Y
Sbjct: 61  PDADLPETQRVVIDTPRLQGSISMLGGRLDDLSLKSYPHETLDPQSQIVRLSPVGPQPNAY 120

Query: 109 QAQSGLTGRDGPDPNPANGPRPLYNVEKDAYVLAEGQNELQVPMT--YTDAAGNTFTKTFV 166
          A  G  T          A  G  +          +  G  +  P+T  + +  G  FT+T
Sbjct: 121 YALYGWTPAG-----ALGYEDVPGANTTWTQVGSALGVDQPVTLQWDNGKGLVFTRTIS 175

Query: 167 LKRGDYAVNVNINVQNAGEKPLEISSFGQLKQSITLPPHLDTGSSNFALHTFRGAAYSTP 226
          +  Y  +V  V+N  + +++++ +G + +  P +L  + F  LH
Sbjct: 176 VD-DHYMFSAQTVENNSGQAVQLAPYIGIVARH-GKPLNLQ---NFFVLHE---GVVGRA 227

Query: 227 DEKYEKYKFDTIAD-----NENLNISSKGGWVAMLQQYFATAWIPHNDGTNNFYTA 277
          D  K  + K+D +A+          + + + GW+  +Y+ T  IP  T
Sbjct: 228 DGKLTETKYDKVAELPQVAREGAQAEVIDAQDQGWIGFTDKYWMTTLIPQQGQPFTSVTK 287

Query: 278 NL-GNGIAAIGYKSQPVLVQPGQTGMNSTLWVGPEIQDKMAAVA-----P 322
          +  G  I          +  Q  V  V  PG  T  ++S  L+  G  +  + + A          P
Sbjct: 288 YVPGADIYQAETREQLVTVPAGATAEVSSRLFAGAKEWETIRAYQNEGATEPTEGAEPPI 347

Query: 323 HLDLTVDYGWLWFISQPLFKLLKWIHSFVGNWGFSSIIITFIVRGIMYPLTKAQYTSMAK 382
          ++D+GW +F+++P+F +L W++ +GN G +II +TF+++ ++ PL  Y SMA+
Sbjct: 348 GFIDSIDWGWFFFLTKPIFTVLHNLNMIGNMGLAIIALTFLKALVLPLAYKSYVSMAR 407

Query: 383 MRMLQPKIQAMRERLGDDKQRISQEMMALYKAQVNPLGGCFPLLIQMPIFLALYYMLMG 442
          M+ LQP+++A+RER GDDK + +EMM LYK ++VNP GC P+LIQ+PIF +LY ++
Sbjct: 408 MKELQPELEALRERAGDDKMLMQREMMRLYKEKQVNPAAGCLPILIQIPIFFSLYKVIFV 467

Query: 443 SVELRQAPFALWIHDLQAQDPYI-----LPILMGVTMFF 477
          ++ELR APF  W+  DLSA DP  I          LPIL+GV+M+
Sbjct: 468 TIELRHAPFFGWLKDLSDPSSIFNFFGLAPWAAPTPTTALIFIGALPILLGVSMWL 527

Query: 478 IQKMSPTTVDTPMQQKIMTFMPVIFTVFLLWFPSGLVLYYIVSNLVTIIQQQLIYR 533
          QK++P  D  Q  I  +MP +F          F SGLVLY+IV+NL+T  QQ +I R
Sbjct: 528 QQKLNPA-PGDKAQAMIFAWMPWVFMFLGHFASGLVLYWIVNNLITFTQQYVIMR 582

```

>ref|ZP_00268613.1| COG0706: Preprotein translocase subunit YidC [Rhodospirillum
rubrum]
Length = 595

Score = 228 bits (581), Expect = 1e-58

Identities = 153/523 (29%), Positives = 261/523 (49%), Gaps = 47/523 (8%)

```

Query: 41  TTAAGSAADQGVPSAGQGKLISVKTDVLDLTINTRGGDVEQALLPAYPKELNSTQPFQLL 100
          T  A  S  + +  A+  I + T  L  +I  RG  ++  L  Y  + ++  P  L
Sbjct: 84  TPGAASLSREEALAADISPRIGIDTARLHGSIRLRGARIDDLSDVDYRETVDPSPEISL 143

Query: 101 ETSP--QFIYQAQSG-LTGRDGPDPNPANGPRPLYNVEKDAYVLAEGQNELQVPMTYTDA 157

```

```

      + P      Y A+ G + G G P      L+ ++ A +      + V +T+ +
Sbjct: 144 LSPPGAPLPYYAEFGWVAGTPGVKVP--DADTLWQADRGALGV-----DAPVTLTWDNGE 196

Query: 158 GNTFTKTFVLKRGDYAVNVNYNVQNAGEKPLEISSFGQLKQSITLPPHLDTGSSNFALHT 217
      G F +      + D+ ++ V+N G      + + +G L I P L+      + LH
Sbjct: 197 GLRFIRKIAIDH-DFMFSITQAVENTGAGAVTLFPYG-LVSRINTPALLNY----YILHE 250

Query: 218 FRGAAYSTPDEKYEKYKFDTIADNENLNISSEKGGWVAMLQQYFATAWIPHNDG--TNNF- 274
      + D ++ K+ + D+ + +S GGW+ + +Y+ TA +      T F
Sbjct: 251 GPLGVF---DGTLKEVKYSALKDDGEVKHTSTGGWVGITDKYWLTAALVTDQSMPTVGRFL 307

Query: 275 YTANLGNGIAAIGYKSQPVLVQPGQTGAMNSTLWVGPEIQDKMAAVAPHL-----DLTVD 329
      Y G      +      V+PG      ++ L+ G +      +      L DL +D
Sbjct: 308 YQPRDGRDGYQADFLGAAFTVEPGGRIETSNHLFSGAKEVKLLDRYTDELGIKNFDLAID 367

Query: 330 YGWLWFISQPLFKLLKWIHSFVGNWGFSSIIITFIVRGIMYPLTKAQYTSMAKMRMLQPK 389
      +GW +F+++P F ++++H +GN G +I+ T +++ + +PL Y SM+KM++LQP+
Sbjct: 368 FGWFYFMTKPFLLSIQFLHGILGNMGLAILAFTVVLKLVFFPLANKSYRSMKMKLLQPE 427

Query: 390 IQAMRERLGDDKQRISQEMMALYKAQKVNPLGGCFPLLIQMPIFLALYYMLMGVSVELRQA 449
      ++ ++ER DD+ R++QEMM+LYK E+VNPL GC P++IQ+P+F ALY +L S+E+R
Sbjct: 428 LKKLQERFKDDRARLNQEMMSLYKKEQVNPLSGCLPIVIQIPVFFALYKVLFVSIEMRHE 487

Query: 450 PFALWIHDLAQDPYYIL-----PILMGVTMFFIQKMSPTTVTDPM 490
      PF WI DL+A DP +      P++MGVTM+ QK++PT DP
Sbjct: 488 PFYGWIRDLAAPDPTTVFNLFGLIPWDPPNMLMLGAWPLIMGVTMWMQKLNPTP-ADPT 546

Query: 491 QQKIMTFMPVIFTVFFLWFPSGLVLYIIVSNLVTIIQQQLIYR 533
      Q KIM F+P++FT F +GLV+Y+ +NL++I QQ +I +
Sbjct: 547 QAKIMMFLPIMFTFMLAHFAAGLVIIYWTWNLLSITQQWVIMK 589

```

>ref|YP_032573.1| hypothetical protein BQ09780 [Bartonella quintana str. Toulouse]
Length = 613

Score = 226 bits (577), Expect = 3e-58

Identities = 155/519 (29%), Positives = 259/519 (49%), Gaps = 67/519 (12%)

```

Query: 61 ISVKTDVLDLTINTRGGDVEQALLPAYPKELNSTQPFQLLETSPQFI--YQAQSGLTGRD 118
      I++KTD L+ +IN G + LL Y ++ P L F Y A+ G T
Sbjct: 90 IAIKTDELEGSINLVGAQFDDLLLKKYRLTVDKKSPEIALLNPKGFTTTTYLAEFGFT--- 146

Query: 119 GPDNPANGPRPLYNVEKDAYVLAEGQNELQVPMT-----YTDAAGNTFTKTFVLKRGDYA 173
      + + + L + D EG N P T Y + G F +T + Y
Sbjct: 147 ---SSSLSAKAL--PQSDTQWQIEGNNTTLPSTPVTLIYNNQGQIFRRTLSVDN-HYM 200

Query: 174 VNVNYNVQNAGEKPLEISSFGQLKQSITLPPHLDTGSSNFALHTFRGAAYSTPDEKYEKY 233
      + +++N +KP+ +SS+ ++ ++ P H + + + LH ++ K EKY
Sbjct: 201 FTIEDSIKNESDKPIYLSSYARVARAAP-PEHTN---ATYLLHEGM-IGIASDSLKTEKY 255

Query: 234 KFDTIAD-NENLNISSEK-----GGWVAMLQQYFATAWIPHNDG--TNNFYTANLGNG 282
      K T+A+ N N + S K GGW+ + +Y+A A IP D T+ F + N
Sbjct: 256 K--TLAELNPNPDNSQKSITFSKNIGGWIGITDKYWAVAVIPPQDKEYTSRFIYFDRNT 313

Query: 283 IAAIGYKSQPVLVQPGQTGAMNSTLWVGPEIQDKMAAVAPHLD-----LTVDYGWL 333
      + V P +T + + L+ G K + H L +D+GW
Sbjct: 314 HYQSDLLGSLLTVPANETKIVTNRLFAGA---KQVEIINHYNQNDLKIKKFALLIDWGW 369

Query: 334 WFISQPLFKLLKWIHSFVGNWGFSSIIITFIVRGIMYPLTKAQYTSMAKMRMLQPKIQAM 393

```

FI++P+F L+ ++ GN+G +I+++T +++ +++PL Y SMA+M+++QP + +
 Sbjct: 370 DFITKPMFSLIDTLYKQTGNFGIAILLVTVLLKTLLFPLANKSYKSMARMKLIQPMLEI 429

Query: 394 RERLGDDKQRISQEMMALYKAQKVNPLGGCFPLLIQMPIFLALYYMLMGVELRQAPFAL 453
 +E+ DD+ + Q ++ LYK +K+NPL GC+P+LIQ PIF ALY +L ++E+R APF
 Sbjct: 430 KEKYPDDRTKQQQAIIELYKTQKINPLAGCWPMLIQFPIFFALYKVLYITIEMRHAPFFG 489

Query: 454 WIHDLAQDPYYIL-----PILMGVTMFFIQKMSPTTVTDPMQOKI 494
 WI DL+A DP + P++MG+TMF +M+P D Q I
 Sbjct: 490 WIQDLAAPDPTSLFNLFLGLLPYTVPTFLMLGAWPLIMGITMFLQMRMNAP-QDQTQAMI 548

Query: 495 MTFMPVIFTVFFLWFPSGLVLYIIVSNLVTIIQQQLIYR 533
 +MPVIFT FP GLV+Y+ +N+++I+QQ ++ +
 Sbjct: 549 FAWMPVIFTFMLASFPVGLVIYWANNILSILQQSILMK 587

>ref|NP_859643.1| conserved hypothetical membrane protein [Helicobacter hepaticus
 ATCC 51449]
 Length = 591

Score = 223 bits (568), Expect = 3e-57
 Identities = 103/231 (44%), Positives = 163/231 (70%), Gaps = 2/231 (0%)

Query: 308 WVGPEIQDKMAAVAPHLDTVDYGLWLFISQPLFKLLKWIHSFVGNWGFSSIIITFIVRG 367
 ++GP+ ++ + L V+YG + F ++PLF LL++++ GNWG++I+++T IVR
 Sbjct: 342 YIGPKEYHELGQIENTLTDVVEYGRITFFAKPLFLLLEYLYDLGCGNWGWAIVLLTLIVRI 401

Query: 368 IMYPLTKAQYTSMAKMRMLQPKIQAMRERLGDDKQRISQEMMALYKAQKVNPLGGCFPLL 427
 ++YPLT SM K++ L PK++ ++ R DD Q++ MM LYK NPLGGC PL+
 Sbjct: 402 VLYPLTYKGMVSMQKLKDLAPKMKDLQTRYKDDPQKLQIHMDLYKKHGANPLGGCLPLI 461

Query: 428 IQMPIFLALYYMLMGVELRQAPFALWIHDLAQDPYYILPILMGVTMFFIQKMSPTTVT 487
 +Q+P+F A+Y +L +VEL+ + + LWI DLSA DPY++LP+LMGV+M+ QK++P+ T
 Sbjct: 462 LQIPVFFAIYRVLHNAVELKSSAWILWITDLSAIDPYFVLPVLMGVSMYISQKLTPSNFT 521

Query: 488 DPMQOKIMTFMPVIFTVFFLW--FPSGLVLYIIVSNLVTIIQQQLIYRGLE 536
 DPMQ+KI +P +FT+FF+ FP+GLVLY+ ++N+ +IIQQ I + +E
 Sbjct: 522 DPMQEKIFKMLPWVFTIFFIIFFPAGLVLYWTINNVSIIQQISINKIME 572

>ref|ZP_00338426.1| COG0706: Preprotein translocase subunit YidC [Silicibacter sp.
 TM1040]
 Length = 615

Score = 220 bits (560), Expect = 3e-56
 Identities = 167/592 (28%), Positives = 280/592 (47%), Gaps = 73/592 (12%)

Query: 2 DSQRNLLVIALLFVSFMIWQAW-----EQDKNPQPQAQQTQTTTTAAGSAADQGVPA 54
 D +NLL+ L SF++ W E+ P + +T T A +AA A
 Sbjct: 10 DQKNKLLALATL--SFLVILGWYFFFPPEEAPQPATEVTETAPQGDTTAPAAAPSAGAA 67

Query: 55 SGQGKLISVKTDVLD----LTINT-----RGGDVEQALLPAYPKELNSTQPFQLE 101
 + + + +T++ + LTI+T +GG ++ L Y + L+ P L
 Sbjct: 68 TAEVDAAAETEITEDVPRLTIDTPRVEGSISLKGGRIDDLRLKDYRETLDSDSPIVTL- 126

Query: 102 TSPQFIYQAQSGLTGRDGPDPNPANGPRPLYNVEKDAYVLAEGQNELQVPMTYTDAAGNTF 161
 SP A L G P N A A + V +T+ + G TF
 Sbjct: 127 LSPAGQPHAYYALYGWAPGAGLGIEDVPTANTLWQAEAGATLTPDTPVTLTWDNGKGLTF 186

Query: 162 TKTFVLKRGDYAVNVNYNVQNAGEKPLEISSFGQLKQSITLPPHLDTGSSNFALHTFRGA 221
 ++ + DY ++ +V N+ + ++ +G L + P +L+ + F LH
 Sbjct: 187 SREVSIDE-DYMFSITQSVTNSSGASVALAPYGTLARHGE-PANLE---NFFVLHE---G 238

Query: 222 AYSTPDEKYEKYKFDTIADNE-----NLNISSKGGWVAMLQQYFATAWIPH-NDGT 271
 D + + +D + D + +N ++ GW+ Y+ + IP +
 Sbjct: 239 VVGMADELSEIDYDDMTDFDPDRDGSRAQVNTVTENGWIGFTGHYWMSTLIPAPGEAF 298

Query: 272 NNFYTANLGNIAAIGYKSPVLVQPGQTGAMNSTLWVGPEI-----QDKMAAVAPHLDL 326
 + I V + G++ + N+ L+ G + + + A + LD
 Sbjct: 299 RAIKYDERRDIYQTDVVLPTVTLAAGESTSANTQLFAGAKEWATIREYERAGIEGFLD- 357

Query: 327 TVDYGWLWFISQPLFKLLKWIHSFVGNWGFSSIIITFIVRGIMYPLTKAQYTSMAKMRML 386
 ++D+GW +F ++P+F +L W+++ +GN G +II +TF+++ +++PL Y SMA+M+ L
 Sbjct: 358 SIDWGWFFFFFTKPIFAVLHNLNAAIGNMGVAIIALTFLKILVFPLAYKSYASMARMKEL 417

Query: 387 QPKIQAMRERLGGDKQRISQEMMALYKAEKVNPLGGCFPLLIQMPIFLALYYMLMGSVEL 446
 QP+++ +RER GDD+Q++ +EMM LYK EKVNP GC P+LIQ+PIF +LY ++ ++EL
 Sbjct: 418 QPEMEKLRERAGDDRQKMQKEMMELYKREKVNPAAGCLPILIQIPIFFSLYKVFVFTLEL 477

Query: 447 RQAPFALWIHDLQAQDP-----YYILPILMGVTMFFIIQKM 481
 R A F DLS DP ILPI+GV+M+ QK+
 Sbjct: 478 RHAAFFGPFQDLSVPDPTSLFNLFGLLPWAAPAPDSLLSLVFIGILPILLGVSMWVQKL 537

Query: 482 SPTTVTDPMQQKIMTFMPVIFTVFFLWFPGLVLYIVSNLVTIIQQQLIYR 533
 +P TD Q+ I +MP +F F SGLV+Y+I +N++T QQ LI R
 Sbjct: 538 NPAP-TDETQRMIFAWMPVWFMLGGFASGLVYVITNNVITFTQQYLIMR 588

>ref|YP_033995.1| hypothetical protein BH12410 [Bartonella henselae str. Houston-1]
 Length = 612

Score = 212 bits (540), Expect = 6e-54

Identities = 145/515 (28%), Positives = 253/515 (49%), Gaps = 59/515 (11%)

Query: 61 ISVKTDVLDLTINTRGGDVEQALLPAYPKELNSTQPFQLLETSPQF--IYQAQSGLTGRD 118
 +++KT+ L+ +IN G + LL Y ++ L F Y A+ G T
 Sbjct: 89 VAIKTNELEGSINLVGAQFDDLLKKYRLTVDKKSSEIALLNPKGFKETYLAIEFGFTSSS 148

Query: 119 GPDNPANGPRPLYNVEKDAYVLAEGQNELQVPMTYTDAAGNTFTKTFVLKRGDYAVNVNY 178
 + +++E + L V + Y + G TF + + Y +
 Sbjct: 149 LSKDALPQSDTRWHIEGNNTTLPST---PVTLIYNNQGQTFRRILSID-DHYMFTIED 204

Query: 179 NVQNAGEKPLEISSFGQLKQSITLPPHLDTGSSNFALHTFRGAAYSTPDE-KYEKYKFDT 237
 ++ N +KP+ +SS+ ++ ++ P H + + + LH G D K EKYK T
 Sbjct: 205 SITNESDKPIYLSSYARVARAAP-PEHTN---ATYLLH--EGMIGIAGDSLKTEKYK--T 256

Query: 238 IAD-NENLNISK-----GGWVAMLQQYFATAWIPHNDG--TNNFYTANLGNIAAI 286
 +A+ N N + K GGWV + +Y+A A IP D T+ F +
 Sbjct: 257 LAELNPNPDNGQKSMTFSKVIGGWGITDKYWAVAVIPPQDKEYTSRFIYFDRQLQTHYQS 316

Query: 287 GYKSQPVLVQPGQTGAMNSTLWVGPEIQDKMAAVAPHLD-----LTVDYGWLWFIS 337
 + V P +T + + L+ G K + H L +D+GW FI+
 Sbjct: 317 DLLGSLLTVAPNETKITNRLFAGA----KQVEIINHYNQNDLKIKKFALLIDWGWDFDIT 372

Query: 338 QPLFKLLKWIHSFVGNWGFSSIIITFIVRGIMYPLTKAQYTSMAKMRMLQPKIQAMRERL 397
 +P+F L+ ++ GN+G +I+++T +++ +++PL Y SMA+M+++QP + ++E+
 Sbjct: 373 KPMFSLIDILYKQTGNFGIAILLVTVLLKTLFPLANKSYKSMARMKLIQPMLEIKEKY 432

Query: 398 GDDKQRISQEMMALYKAEKVNPLGGCFPLLIQMPIFLALYYMLMGSVELRQAPFALWIHD 457
 +D+ + Q ++ LYK +K+NPL GC+P+L+Q PIF ALY +L ++E+R APF WI D
 Sbjct: 433 PEDRTKQQQAIIELYKTQKINPLAGCWPMVLVQFPFIFFALYKVLYITIEMRHAPFFGWIQD 492

Query: 458 LSAQDPYYIL-----PILMGVTMFFIQKMSPTTVTDPMQQKIMTFM 498
 L+A DP + P++MG+TMF +M+P D Q I +M
 Sbjct: 493 LAAPDPSTSLFNLFGLLPYTVPAFLMLGAWPLIMGITMFLQMRMNPAP-QDQTQAMIFAWM 551

Query: 499 PVIFTVFFLWFPSGLVLYIIVSNLVTIIQQQLIYR 533
 P++FT FP GLV+Y+ +N++++IQQ ++ +
 Sbjct: 552 PIVFTFMLASFPVGLVIYWANNILSMIQQGIMMK 586

Database: Unfinished Ehrlichia ruminantium str. Welgevonden
 Posted date: Jul 9, 2004 7:16 PM
 Number of letters in database: 314,482
 Number of sequences in database: 893

Lambda	K	H
0.320	0.135	0.409

Gapped

Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1
 Number of Hits to DB: 13,131,529
 Number of Sequences: 2112941
 Number of extensions: 560667
 Number of successful extensions: 1438
 Number of sequences better than 10.0: 11
 Number of HSP's better than 10.0 without gapping: 10
 Number of HSP's successfully gapped in prelim test: 1
 Number of HSP's that attempted gapping in prelim test: 1387
 Number of HSP's gapped (non-prelim): 15
 length of query: 548
 length of database: 228,314,449
 effective HSP length: 123
 effective length of query: 425
 effective length of database: 138,579,553
 effective search space: 58896310025
 effective search space used: 58896310025
 T: 11
 A: 40
 X1: 16 (7.4 bits)
 X2: 38 (14.6 bits)
 X3: 64 (24.7 bits)
 S1: 41 (21.8 bits)
 S2: 73 (32.7 bits)